OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: December 6, 2004, 13:34:19 ; Search time 195.614 Seconds
                   (without alignments)
                   278.934 Million cell updates/sec

Title: US-08-836-455-4
Perfect score: 816
Sequence: 1 MECSWVFLFLLSITTGVHSQ..........TVSSAKTTPPVYPLVPGSL 153

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5
Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Post-processing: Minimum Match 0%
Maximum DB seq length: 0   Maximum Match 100%
Minimum DB seq length: 0   Listing first 45 summaries
Maximum DB seq length: 200000000

Database :   Published Applications AA:*
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB ID	Description
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2	816	100.0	153	14	US-10-367-506-4	Sequence 4, Appli
3	574.5	70.4	468	10	US-09-795-515-7	Sequence 7, Appli
4	574.5	70.4	468	15	US-10-704-352-7	Sequence 7, Appli
5	574.5	70.4	468	15	US-10-704-071-7	Sequence 7, Appli
6	574.5	70.4	468	16	US-10-682-845-38	Sequence 38, Appl
7	574.5	70.4	468	17	US-10-703-963-7	Sequence 7, Appl
8	565	69.2	468	17	US-10-742-405-12	Sequence 12, Appl
9	560	68.7	464	14	US-10-216-484-9	Sequence 9, Appli
10	560.5	68.7	464	14	US-10-384-933-9	Sequence 9, Appli
11	554.5	68.0	464	9	US-09-903-327A-5	Sequence 6, Appli
12	554.5	68.0	456	9	US-09-903-327A-2	Sequence 2, Appli
13	554.5	68.0	493	9	US-09-903-327A-13	Sequence 13, Appl
14	554.5	68.0	153	9	US-09-903-327A-12	Sequence 12, Appl
15	554.5	68.0	597	9	US-09-903-327A-11	Sequence 11, Appl
16	554.5	68.0	613	9	US-09-903-327A-14	Sequence 14, Appl
17	552.5	67.7	136	14	US-10-160-232-88	Sequence 88, Appl
18	543	66.5	238	14	US-10-336-210-3	Sequence 3, Appli
19	543	66.5	272	14	US-10-336-210-7	Sequence 7, Appli
20	540	66.2	135	14	US-10-244-821-91	Sequence 91, Appl
21	539.5	66.1	180	9	US-09-748-960-6	Sequence 6, Appli
22	536	65.7	152	16	US-10-642-120-2	Sequence 2, Appli
23	536	65.7	152	16	US-10-642-060-2	Sequence 2, Appli
24	536	65.7	152	16	US-10-642-122-2	Sequence 2, Appli
25	536	65.7	152	16	US-10-642-124-2	Sequence 2, Appli
26	536	65.7	152	16	US-10-621-269-2	Sequence 2, Appli
27	536	65.7	152	16	US-10-620-850-2	Sequence 2, Appli
28	536	65.7	152	16	US-10-642-118-2	Sequence 2, Appli
29	536	65.7	152	17	US-10-642-117-2	Sequence 2, Appli
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32	536	65.7	237	14	US-10-336-210-2	Sequence 2, Appli
33	536	65.7	271	14	US-10-336-210-6	Sequence 6, Appli
34	536	65.7	152	17	US-10-642-116-2	Sequence 2, Appli
35	530	65.0	139	14	US-09-509-098-4	Sequence 4, Appli
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37	528	64.7	139	10	US-09-269-921-126	Sequence 126, App
38	528	64.7	139	10	US-09-269-921-126	Sequence 126, App
39	528	64.7	139	13	US-09-509-098-98	Sequence 98, Appl
40	528	64.7	139	14	US-11-006-773-13	Sequence 13, Appl
41	522.5	64.0	140	10	US-10-218-253-126	Sequence 126, App
42	522.5	64.0	140	14	US-09-905-928-6	Sequence 6, Appli
43	522.5	64.0	164	17	US-10-096-964-6	Sequence 6, Appli
43	522	64.0	135	14	US-10-471-475A-23	Sequence 23, Appl
44	522	64.0	135	14	US-10-389-155-60	Sequence 60, Appl
45	522	64.0	135	15	US-10-389-417-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-09-861-294-4

; Sequence 4, Application US/09861294
; Patent No. US2002009819OA1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 3041420000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 4
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-09-861-294-4

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Best Local Similarity   100.0%;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Pred. No. 7.8e-61;

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RESULT 2
US-10-367-506-4
; Sequence 4, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; APPLICANT: Kenneth A. FOON
; FILE REFERENCE: 30414200620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-367-506-4

Query Match   100.0%; Score 816; DB 14; Length 153;
Best Local Similarity   100.0%; Pred. No. 7.8e-61;
Matches 153; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
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RESULT 3
US-09-795-515-7
; Sequence 7, Application US/09795515
; Publication No. US20003003645A1
; GENERAL INFORMATION:
;  APPLICANT: Adair, John R.
;  APPLICANT: Athwal, Diljeet S.
;  APPLICANT: Emtage, John S.
;  TITLE OF INVENTION: Humanised Antibodies
;  NUMBER OF SEQUENCES: 30
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645Alris
;  STREET: One Liberty Place - 46th Floor
;  CITY: Philadelphia
;  STATE: PA
;  COUNTRY: USA
;  ZIP: 19103
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk

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;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/09/795,515
;  FILING DATE:
;  CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 08/846,658
;  FILING DATE: 01-MAY-1997
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Trujillo, Doreen Yatko
;  REGISTRATION NUMBER: 35,719
;  REFERENCE/DOCKET NUMBER: CARP-0057
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (215) 568-3100
;  TELEFAX: (215) 568-3439
;  INFORMATION FOR SEQ ID NO: 7:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 468 amino acids
;  TYPE: amino acid
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-09-795-515-7

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US-10-704-352-7
; Sequence 7, Application US/10704352
; Publication No. US20040071693A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/704,352
; FILING DATE: 07-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE: 28-FEB-2001
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: December 6, 2004, 13:29:00 ; Search time 16.4295 seconds
                                                (without alignments)
                                                617.586 Million cell updates/sec

Title: US-08-836-455-4
Perfect score: 816
Sequence: 1 MECSWVFLPLLSITTGVHSQ.........TVSSAKTTPPPVYPLVPGSL 153

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	816	100.0	153	US-09-096-244-4	Sequence 4, Appl
2	574.5	70.4	468	US-08-303-569B-7	Sequence 7, Appli
3	574.5	70.4	468	US-08-116-247-7	Sequence 7, Appli
4	574.5	70.4	468	US-09-795-515-7	Sequence 7, Appli
5	574.5	70.4	468	US-08-348-224-7	Sequence 7, Appli
6	568.5	69.7	151	US-08-513-968-34	Sequence 34, Appl
7	568	69.6	561	US-09-192-545-2	Sequence 2, Appli
8	565	69.2	140	US-09-724-138-44	Sequence 44, Appl
9	554	68.0	464	US-08-353-400-36	Sequence 36, Appl
10	541.5	66.4	138	US-09-254-180C-143	Sequence 143, App
11	535	65.6	235	US-08-444-644-19	Sequence 19, Appl
12	535	65.6	235	US-08-232-246A-19	Sequence 19, Appl
13	534	65.4	139	US-08-253-877C-8	Sequence 8, Appli
14	534	65.4	139	US-08-452-164A-8	Sequence 8, Appli
15	533	65.3	138	US-08-603-024-2	Sequence 2, Appli
16	532	65.2	235	US-08-444-644-28	Sequence 28, Appl
17	532	65.2	235	US-09-444-644-42	Sequence 42, Appl
18	532	65.2	235	US-08-232-246A-42	Sequence 42, Appl
19	532	65.2	235	US-08-232-246A-28	Sequence 28, Appl
20	531.5	65.1	136	PCT-US93-11611-4	Sequence 4, Appli
21	530	65.0	139	US-09-269-921-105	Sequence 105, App
22	528	64.7	139	US-09-269-921-126	Sequence 126, App
23	525.5	64.4	140	US-08-579-378A-4	Sequence 4, Appli
24	525.5	64.4	140	PCT-US93-11612-4	Sequence 4, Appli
25	522.5	64.0	140	US-08-476-275-6	Sequence 6, Appli
26	522.5	64.0	140	US-08-475-813-6	Sequence 6, Appli
27	522	64.0	135	US-07-634-278-69	Sequence 69, Appl
28	522	64.0	135	US-08-477-728-69	Sequence 69, Appl
29	522	64.0	135	US-08-474-040-69	Sequence 69, Appl
30	522	64.0	135	US-08-487-200-69	Sequence 69, Appl
31	522	64.0	135	US-08-484-537-69	Sequence 69, Appl
32	520.5	63.8	140	US-08-475-815B-11	Sequence 131, Appl
33	520.5	63.8	219	US-09-254-180C-131	Sequence 131, App
34	520.5	63.8	219	US-09-254-180C-181	Sequence 181, App
35	518	63.5	233	US-08-444-644-33	Sequence 33, Appl
36	518	63.5	233	US-08-232-246A-33	Sequence 33, Appl
37	516.5	63.3	150	US-08-400-115-2	Sequence 2, Appli
38	512	62.7	137	US-09-647-468-153	Sequence 153, App
39	512	62.7	219	US-09-647-468-154	Sequence 154, App
40	511.5	62.7	445	US-09-254-180C-180	Sequence 180, App
41	511.5	62.6	139	US-08-353-400-33	Sequence 33, Appl
42	511	62.6	139	US-08-137-117D-35	Sequence 35, Appl
43	511	62.6	139	US-08-436-717-35	Sequence 35, Appl
44	511	62.6	139	US-08-656-586-4	Sequence 4, Appli
45	510	62.5	137	US-08-392-419-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-096-244-4
Sequence 4, Application US/09096244
; Patent No. 6274143
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
; TITLE OF INVENTION: HMFG-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 11D10
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MORRISON & FOERSTER
;   STREET: 755 PAGE MILL ROAD
;   CITY: PALO ALTO
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304-1018
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/096,244
;   FILING DATE:
;   CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Polizzi, Catherine M.
;   REGISTRATION NUMBER: 40,130
;   REFERENCE/DOCKET NUMBER: 30414-20006.00
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 813-5600
;   TELEFAX: (650) 494-0792
;   TELEX: 706141
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 153 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-096-244-4

Query Match   100.0%; Score 816; DB 3; Length 153;
Best Local Similarity   100.0%; Pred. No. 9.8e-61;
Matches 153; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISLLTSEDSAVYFCARGNW 120
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Qy 121 EGALDYWGQGTSVTVSSAKTTPPPVYPLVPGSL 153
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RESULT 2
US-08-303-569B-7
; Sequence 7, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
;   APPLICANT: Adair, John R.
;   APPLICANT: Athwal, Diljeet S.
;   APPLICANT: Emtage, John S.
;   TITLE OF INVENTION: Humanised Antibodies
;   NUMBER OF SEQUENCES: 31
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
;   STREET: One Liberty Place - 46th Floor
;   CITY: Philadelphia
;   STATE: PA
;   COUNTRY: USA
;   ZIP: 19103
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/303,569B
;   FILING DATE: 07-SEP-1994
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Trujillo, Doreen Yatko
;   REGISTRATION NUMBER: 35,719
;   REFERENCE/DOCKET NUMBER: CARP-0032
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (215) 568-3100
;   TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 468 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-303-569B-7

  Query Match   70.4%; Score 574.5; DB 2; Length 468;
  Best Local Similarity   74.8%; Pred. No. 4e-40;
  Matches 113; Conservative   8; Mismatches 29; Indels   1; Gaps   1;

Qy   1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
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Db   1 MERHWIFLLLLSVTAGVHSQVQLQQSGAELARPGASVKMSCKASGYTFTRYTMHWVKQRP 60

Qy   61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISLLTSEDSAVYFCAR-GN 119
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Db   61 GQGLEWIGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSLTSEDSAVYYCARYD   120

Qy 120 WEGALDYWGQGTSVTVSSAKTTPPPVYPLVP 150
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Db 121 DHYCLDYWGQGTTLTVSSAKTTAPSVYPLAP 151

RESULT 3
US-08-116-247-7
; Sequence 7, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
;   APPLICANT: Jolliffe, Linda K.

;   APPLICANT: Zivin, Robert A.
;   APPLICANT: Adair, John R.
;   APPLICANT: Athwal, Diljeet S.
;   TITLE OF INVENTION: CD3 Specific Recombinant Antibody
;   NUMBER OF SEQUENCES: 29
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5929212ris
;   STREET: One Liberty Place - 46th Floor
;   CITY: Philadelphia
;   STATE: PA
;   COUNTRY: USA
;   ZIP: 19103
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/116,247
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/743,377
;   FILING DATE: 10-OCT-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Paintin, Francis A.
;   REGISTRATION NUMBER: 19,386
;   REFERENCE/DOCKET NUMBER: CARP-0011
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (215) 568-3100
;   TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 468 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-116-247-7

  Query Match   70.4%; Score 574.5; DB 2; Length 468;
  Best Local Similarity   74.8%; Pred. No. 4e-40;
  Matches 113; Conservative   8; Mismatches 29; Indels   1; Gaps   1;

Qy   1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
         ||:|||| ||||:||||||||||||||:|||||||||||||||||||:|||||||||||
Db   1 MERHWIFLLLLSVTAGVHSQVQLQQSGAELARPGASVKMSCKASGYTFTRYTMHWVKQRP 60

Qy   61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISLLTSEDSAVYFCAR-GN 119
         |||||||| | ||||||||||||||||||| :|||||||| :|||||||||||||| :||
Db   61 GQGLEWIGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSLTSEDSAVYYCARYD   120

Qy 120 WEGALDYWGQGTSVTVSSAKTTPPPVYPLVP 150
         ||||||||||||:||||||||||| ||||
Db 121 DHYCLDYWGQGTTLTVSSAKTTAPSVYPLAP 151

RESULT 4
US-09-795-515-7
; Sequence 7, Application US/09795515
; Patent No. 6632927
; GENERAL INFORMATION:
;   APPLICANT: Adair, John R.
;   APPLICANT: Athwal, Diljeet S.
;   APPLICANT: Emtage, John S.
;   TITLE OF INVENTION: Humanised Antibodies
;   NUMBER OF SEQUENCES: 30
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6632927ris
;   STREET: One Liberty Place - 46th Floor
;   CITY: Philadelphia
;   STATE: PA
;   COUNTRY: USA
;   ZIP: 19103

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 6, 2004, 13:29:00 ; Search time 54.9362 Seconds
                                                  (without alignments)
                                                  999.078 Million cell updates/sec

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Perfect score: 816
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Scoring table:
Scoring table: BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                    Maximum Match 100%
                    Listing first 45 summaries

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                    7: geneseqp2003bs:*
                    8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	602	73.8	159	2	AAP93079	Aap93079 Heavy cha
6	586	71.8	467	5	AAE38408	Aae38408 Mouse vir
7	574.5	70.4	468	2	AAR13061	Aar13061 Monoclona
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9	572.5	70.2	148	8	ADM79825	Adm79825 Mouse IgG
10	568	69.6	561	2	AAY17415	Aay17415 Mouse imm
11	565	69.2	140	1	AAP94780	Aap94780 2 H7 VH g
12	565	69.2	140	2	AAW10242	Aaw10242 Heavy cha
13	565	69.2	140	2	AAW10588	Aaw10588 2H7 antib
14	565	69.2	140	2	AAW16343	Aaw16343 2H7 heavy
15	565	69.2	140	2	AAW41070	Aaw41070 Mouse 2H7
16	565	69.2	140	2	AAW47513	Aaw47513 Mouse 2H7
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18	565	69.2	140	2	AAW89540	Aaw89540 Mouse ant
19	565	69.2	140	4	AAB98092	Aab98092 2H7 heavy
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21	565	69.0	463	2	AAW14939	Aaw14939 3F4 (Chim
22	563	69.0	463	2	AAW14940	Aaw14940 3F4 (Chim
23	563	69.0	464	2	AAW14941	Aaw14941 3F4 Human
24	563	69.0	464	2	AAW14938	Aaw14938 Murine an
25	563	69.0	469	2	AAR40384	Aar40384 Monoclona
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27	561.5	68.8	360	6	ABB82833	Abb82833 Antibody
28	561.5	68.8	470	2	AAB08026	Aab08026 A dimeric
29	561.5	68.8	470	2	AAE27923	Aae27923 Human C2B
30	561.5	68.8	470	1	ABB82832	Abb82832 Antibody
31	561	68.8	140	1	AAP70627	Aap70627 Sequence
32	560.5	68.7	464	2	AAW83041	Aaw83041 Anti-Ras
33	560.5	68.7	464	3	AAB14747	Aab14747 Mouse ant
34	560.5	68.7	464	2	AAW90897	Aaw90897 Murine an
35	560.5	68.7	464	5	ABB74912	Abb74912 Humanised
36	554.5	68.0	464	5	ABB74866	Abb74866 Humanised
37	554.5	68.0	438	2	AAE18372	Aae18372 Human pen
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39	554.5	68.0	456	5	AAE18370	Aae18370 Human pen
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41	554.5	68.0	464	2	AAR76088	Aar76088 MAb 55.1.
42	554.5	68.0	493	5	AAE18379	Aae18379 Human N-t
43	554.5	68.0	493	5	ABG76354	Abg76354 Mouse DAV
44	554.5	68.0	510	5	AAE18378	Aae18378 Human N-t
45	554.5	68.0	510	5	ABG76353	Abg76353 Mouse DAV

ALIGNMENTS

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ID   AAW27120 standard; protein; 153 AA.
XX
AC   AAW27120;
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DT   25-MAR-2003 (revised)
DT   04-JAN-1998 (first entry)
XX
DE   Murine monoclonal anti-idiotype antibody 11D10 VH region.
XX
KW   Monoclonal antibody 11D10; anti-idiotype antibody 11D10 VH region.
KW   human milk fat globule; HMFG; tumour; breast cancer; vaccine.
XX
OS   Mus musculus.
XX
FH   Key   Location/Qualifiers
FH
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FT   /label= Sig_peptide
FT   Protein   20..153
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FT   Region   20..49
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FT   /note= "framework region 1"
FT   Region   50..54
FT   /label= CDR1
FT   /note= "complementarity determining region 1"
FT   Region   55..68
FT   /label= FR2
FT   /note= "framework region 2"
FT   Region   69..85
FT   /label= CDR2
FT   /note= "complementarity determining region 2"
FT   Region   86..117
FT   /label= FR3
FT   /note= "framework region 3"
FT   Region   118..126
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FT   /note= "framework region 4"
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FT   /label= Constant
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PN   WO9722699-A2.
XX
PD   26-JUN-1997.

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PF   19-DEC-1996; 96WO-US020757.
XX
PR   20-DEC-1995; 95US-00575762.
PR   26-JAN-1996; 96US-0059196S.
PR   13-DEC-1996; 96US-00766350.
XX
PA   (KENT ) UNIV KENTUCKY.
XX
PI   Chatterjee M, Foon KA, Chatterjee SK;
XX
DR   N-PSDB; AAT85150.
XX
WPI; 1997-341690/31.
XX
PT   Monoclonal anti-idiotype antibody 11D10 - elicits immune response against
PT   human milk fat globule disease associated tumours, especially breast
PT   cancer.
XX
PN   Claim 10; Page 94-95; 130pp; English.
XX
CC   This polypeptide sequence comprises the heavy chain variable region (VH)
CC   of monoclonal anti-idiotype antibody 11D10 produced by hybridoma cell
CC   line ATCC 12020. 11D10 was obtained by immunising naive mice with MC-10
CC   anti-HMFG antibody to obtain an anti-idiotype response. It elicits an
CC   immune response against a specific epitope of a high mol.wt. mucin of
CC   human milk fat globule (HMFG). It induces an immunological response to
CC   HMFG in mice, rabbits, monkeys and patients with advanced HMFG-associated
CC   tumours. Pharmaceutical compositions and vaccines comprising 11D10, 11D10
CC   polypeptides and/or 11D10 polynucleotides (see also AAT85149-50) are
CC   claimed. Also claimed are diagnostic kits and methods of using 11D10,
CC   11D10 polypeptides and/or 11D10 polynucleotides, including methods of
CC   treating HMFG-associated disease and in claimed kits to detect or
CC   quantify anti-HMFG antibody. (Updated on 25-MAR-2003 to correct PR
CC   field.)
XX
SQ   Sequence 153 AA;

Query Match             100.0%;  Score 816;  DB 2;  Length 153;
Best Local Similarity   100.0%;  Pred. No. 1.1e-54;
Matches 153; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy    1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
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Db    1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60

Qy   61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120

Qy  121 EGALDYWGQGTSVTVSSAKTTPPPVYPLVPGSL 153
          |||||||||||||||||||||||||||||||||
Db  121 EGALDYWGQGTSVTVSSAKTTPPPVYPLVPGSL 153


RESULT 2
AC   AAW87594
ID   AAW87594 standard; protein; 153 AA.
XX
DT   16-MAR-1999  (first entry)
XX
DE   Antibody 11D10 heavy chain variable region.
XX
KW   Murine; mouse; antibody; heavy chain; variable region; anti-idiotype;
KW   human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
XX
OS   Mus sp.
XX
FH   Key            Location/Qualifiers
FT   Peptide        1..19
FT                  /note= "signal peptide"
FT   Protein        20..153
FT                  /note= "mature protein"
FT   Region         20..49
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FT   Domain         50..54
FT                  /label= CDR1
FT                  /note= "complementarity determining region 1"
FT   Region         55..68
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FT   Domain         69..85
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FT   Domain         118..126
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FT   Region         127..137
FT                  /label= framework_4
XX
PN   WO9856419-A1.
XX
PD   17-DEC-1998.
XX
PF   12-JUN-1998; 98WO-US012250.
XX
PR   13-JUN-1997; 97US-0049540P.
PR   11-JUN-1998; 98US-00096244.
XX
PA   (KENT ) UNIV KENTUCKY RES FOUND.
XX
PI   Chatterjee M, Foon KA;
XX
DR   N-PSDB; AAV83773.
XX
WPI; 1999-060029/05.
XX
PT   Delaying development of, or treating, HMFG-associated tumours - using
PT   anti-idiotype antibody 11D10 raised against antibodies to human milk fat
PT   globule protein.
XX
PN   Disclosure; Fig 2; 54pp; English.
XX
CC   This sequence represents the heavy chain variable region of the murine
CC   antibody 11D10. This anti-idiotype antibody is used to delay the
CC   development of, or treat, a human milk fat globule (HMFG) associated
CC   tumour in an individual having low tumour burden. The antibody 11D10 is
CC   used to prevent the recurrence of HMFG-associated tumours e.g. ovarian,
CC   non-small cell lung and pancreatic carcinoma, especially for treating
CC   breast tumours
XX
SQ   Sequence 153 AA;

Query Match             100.0%;  Score 816;  DB 2;  Length 153;
Best Local Similarity   100.0%;  Pred. No. 1.1e-54;
Matches 153; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy    1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
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Db    1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60

Qy   61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
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Db   61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120

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Db  121 EGALDYWGQGTSVTVSSAKTTPPPVYPLVPGSL 153


RESULT 3
AC   AAO16293
ID   AAO16293 standard; protein; 153 AA.
XX
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 13:38:19 ; Search time 2367.26 Seconds
(without alignments)
7096.283 Million cell updates/sec

Title: US-08-836-455-3
Perfect score: 461
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 32822875 seqs, 1821965908 residues
Total number of hits satisfying chosen parameters: 65645750

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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4	320.8	69.6	941	2	BF138189	BF138189 601781314
5	320.2	69.5	667	6	BY724790	BY724790 BY724790
6	319.6	69.3	1576	3	AK007918	AK007918 Mus muscu
7	316.6	68.7	767	3	BF165456	BF165456 601777347
8	316.4	68.6	794	4	BI150371	BI150371 602915205
9	315.6	68.5	745	4	BG871607	BG871607 602790090
10	315.6	68.5	546	6	CA576594	CA576594 K0647B06-
11	311.2	67.5	771	2	BF140551	BF140551 601787584
12	309.6	67.2	529	6	CA576389	CA576389 K0644A12-
13	308.6	66.9	616	2	BF136295	BF136295 601781413
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15	308.4	66.9	838	7	CO555369	CO555369 AGENCOURT
16	308	66.8	655	7	CF912433	CF912433 A063ZA03-
17	306.6	66.5	700	2	BF540088	BF540088 602050325
18	305	66.2	644	2	BE281961	BE281961 601099518
19	305	66.2	793	2	BF136093	BF136093 601783539
20	305	66.2	891	2	BF138460	BF138460 601782916
21	303.4	65.8	756	7	CO558337	CO558337 AGENCOURT
22	303	65.7	955	5	BQ947728	BQ947728 AGENCOURT
23	302.6	65.6	469	5	CA574907	CA574907 K062ZH02-
24	301.6	65.4	690	4	BG968682	BG968682 602835513
25	301.6	65.4	724	4	BG962137	BG962137 602826902
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27	300.4	65.2	767	7	CO565860	CO565860 AGENCOURT
28	299.8	65.0	604	2	BF140035	BF140035 601791175
29	298.4	64.7	538	6	CA578968	CA578968 K0731A04-
30	297.4	64.5	540	6	CA579750	CA579750 K0741H07-
31	296.8	64.4	610	7	CF912857	CF912857 A063BH09-
32	296.8	64.4	724	6	CA570382	CA570382 K0505G11-
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38	293	63.6	477	4	BG966397	BG966397 602832896
39	293	63.6	612	4	BF168514	BF168514 601775412
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ALIGNMENTS

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LOCUS   BE284158   739 bp   mRNA   linear   EST 13-JUL-2000
DEFINITION   601099428F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491766 5',
             mRNA sequence.
ACCESSION   BE284158
VERSION   BE284158.1 GI:9160900
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 739)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbe-r@mail.nih.gov
             Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM8536 row: h column: 07
             High quality sequence stop: 535.

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                     Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match   73.3%; Score 337.8; DB 2; Length 739;
Best Local Similarity   84.1%;
Matches 381; Conservative   0; Mismatches   72; Indels   0; Gaps   0;
Pred. No. 9.6e-90;

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Qy     61 GCTTATCTACAGCAGTCTCTGGGGGCTCGGGGGCCTGAGCGGGTCTGGGGGCCTCAGTGAAGAGTCC 120
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Qy    241 CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCTCCAGCACAGCCCTACATG 300
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Qy    301 CAGATCAGCAGCCTGACATCTGCGGTCTCTATTTTCTGTGCAAGAGAGGGAACTGG 360
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Qy    361 GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACG 420
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Qy    421 ACACCCCCACCCGTCTATCCACTGTCCCTGGA 453
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Db    433 ACACCCCCATCTGTCTATCCACTGGCCCCTGGA 465
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LOCUS       BG518664                892 bp    mRNA      linear      EST 02-APR-2001
DEFINITION  602578528F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491766 5',
            mRNA sequence.
ACCESSION   BG518664
VERSION     BG518664.1    GI:13513763
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 892)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM8536 row: h column: 07
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FEATURES             Location/Qualifiers
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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ORIGIN
Query Match        381;  Best Local Similarity  70.9%;  Score 326.8;  DB 4;  Length 892;
Best Local Similarity   83.9%;  Pred. No. 2e-86;
Matches 381;  Conservative   0;  Mismatches  72;  Indels   1;  Gaps   1;
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Db    93 GTTCAGCGTGCGAGCAGTCTCTGGAGCTGGGCGGAGGGCCTGGGGGCTTCAGTGAACGATGTC 152

Qy   120 CTGCAAGGCTTCTCGGCTACTACACAATTGACCAGTTACATATGCACTGGGTAAAGCAGACACC 179
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Qy   240 TCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCTCCAGCACAGCCCTACAT 299
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LOCUS       BY724721                637 bp    mRNA      linear      EST 17-DEC-2002
DEFINITION  BY724721 RIKEN full-length enriched, adult male aorta and vein Mus
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ACCESSION   BY724721
VERSION     BY724721.1    GI:27137848
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 637)
AUTHORS     Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
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            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
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            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
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            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
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            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: December 6, 2004, 15:14:29 ; Search time 687.898 Seconds
            (without alignments)
            3682.388 Million cell updates/sec

Title: US-08-836-455-3
Perfect score: 461
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Scoring table: IDENTITY_NUC
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Searched: 3694831 seqs, 2747406616 residues
Total number of hits satisfying chosen parameters: 7389662

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Database :   Published_Applications_NA.*
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SUMMARIES

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3	337.8	73.3	1406	18	US-10-742-405-11	Sequence 11, Appli
4	327.2	71.0	409	14	US-10-160-232-7	Sequence 7, Appli
5	326.6	70.8	736	13	US-10-006-773-12	Sequence 12, Appl
6	311.6	67.6	1570	17	US-10-682-845-39	Sequence 39, Appl
7	310	67.2	1570	10	US-09-795-515-6	Sequence 6, Appli
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9	310	67.2	1570	18	US-10-703-963-6	Sequence 6, Appli
10	297.2	64.5	9199	10	US-09-911-692-3	Sequence 3, Appli
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12	297.2	64.5	9209	10	US-09-905-928-2	Sequence 2, Appli
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14	297.2	64.5	9209	15	US-10-238-681-3	Sequence 3, Appli
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41	287.4	62.3	519	17	US-10-621-269-1	Sequence 1, Appli
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-09-861-294-3

; Sequence 3, Application US/09861294
; Patent No. US2002009819A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(461)
; NAME/KEY: sig_peptide
; LOCATION: (1)...(57)
; NAME/KEY: mat_peptide
; LOCATION: (58)...(461)
US-09-861-294-3

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Best Local Similarity   100.0%; Pred. No. 5.1e-140;
Matches   461; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 2

US-10-367-506-3

; Sequence 3, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 30414200620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
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; SEQ ID NO 3
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; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
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US-10-742-405-11

; Sequence 11, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:
; APPLICANT: Bowman, Edward P.
; APPLICANT: Chan, Jason R.
; APPLICANT: Moore, Kevin
; APPLICANT: Nguyen, Nhung
; APPLICANT: Churakova, Tatyana
; APPLICANT: Chen, Shi-Juan
; APPLICANT: Cua, Daniel J.
; TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
; FILE REFERENCE: DX01578K
; CURRENT APPLICATION NUMBER: US/10/742,405
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 1406
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-742-405-11

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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_02:*
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              2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	581	71.2	463	2	Q99LC4	Q99lc4 mus musculu
3	575	70.5	465	2	Q6PJB2	Q6pjb2 mus musculu
4	575	70.5	465	2	AAH18280	Aah18280 mus musculu
5	569	69.7	465	2	Q99L25	Q99l25 mus musculu
6	561.5	68.8	464	2	Q6PF95	Q6pf95 mus musculu
7	561.5	68.8	464	2	AAH57672	Aah57672 mus muscu
8	553.5	67.8	472	2	Q6PJA7	Q6pja7 mus musculu
9	553.5	67.8	472	2	AAH18535	Aah18535 mus muscu
10	549.5	67.3	168	2	Q8VDC9	Q8vdc9 mus musculu
11	548.5	67.2	470	2	Q7TMK1	Q7tmk1 mus musculu
12	544	66.7	613	2	Q8VCX7	Q8vcx7 mus musculu
13	526.5	64.5	481	2	Q91WT1	Q91wt1 mus musculu
14	524.5	64.3	474	2	Q8R3H6	Q8r3h6 mus musculu
15	523.5	64.2	140	1	HV02_MOUSE	Hv02 mouse
16	521	63.8	482	2	P01746	P01746 mus musculu
17	518.5	63.5	482	2	Q8K172	Q8k172 mus musculu
18	516.5	63.3	614	2	Q7TMT6	Q7tmt6 mus musculu
19	515.5	63.2	489	2	Q8VCX4	Q8vcx4 mus musculu
20	514	63.0	468	2	Q99L31	Q99l31 mus musculu
21	506.5	62.1	136	2	Q7TPE3	Q7tpe3 mus musculu
22	499	61.2	142	2	Q92401	Q924q1 mus musculu
23	494.5	60.6	480	2	Q8K024	Q8k024 mus musculu
24	493	60.4	481	2	Q8VCV5	Q8vcv5 mus musculu
25	493	60.4	139	1	HV07_MOUSE	Hv07 mouse
26	489	59.9	488	2	Q91WR1	Q91wr1 mus musculu
27	482	59.1	143	2	Q8KOF2	Q8kof2 mus musculu
28	479.5	58.8	481	2	Q924R0	Q924r0 mus musculu
29	478	58.6	481	2	Q91WT3	Q91wt3 mus musculu
30	477.5	58.5	464	2	Q924R4	Q924r4 mus musculu
31	474	58.1	145	2	Q924P7	Q924p7 mus musculu
32	474	58.1	145	2	Q924R1	Q924r1 mus musculu
33	473.5	58.0	140	2	Q924P8	Q924p8 mus musculu
34	473.5	58.0	146	2	Q924O3	Q924o3 mus musculu
35	472	57.8	145	2	Q924O6	Q924o6 mus musculu
36	471	57.7	143	2	Q924P9	Q924p9 mus musculu
37	470	57.6	137	1	HV11_MOUSE	Hv11 mouse
38	469	57.5	145	2	Q924Q9	Q924q9 mus musculu
39	467	57.2	145	2	P01755	P01755 mus musculu
40	466.5	57.2	142	2	Q924Q7	Q924q7 mus musculu
41	466.5	57.2	146	2	Q924Q2	Q924q2 mus musculu
42	465	57.0	143	2	Q924Q0	Q924q0 mus musculu
43	465	56.9	143	2	Q924P6	Q924p6 mus musculu
44	464	56.9	143	2	Q924R7	Q924r7 mus musculu
45	464	56.9	145	2	Q924R3	Q924r3 mus musculu

ALIGNMENTS

RESULT 1
ID   Q9D8L4   PRELIMINARY;   PRT;   473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   RIKEN FANTOM Consortium;
DE   "Functional annotation of a full-length mouse cDNA, RIKEN full-length enriched
DE   library, clone:1810060009 product:immunoglobulin heavy chain 6 (heavy
DE   chain of IgM), full insert sequence.
GN   Name=Igh-1a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RP   STRAIN=C57BL/6J; TISSUE=Pancreas;
RP   The FANTOM Consortium;
RA   The RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RESULT 2
Q99LC4

RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa Y., Ozawa R., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira S., Hayashizaki Y.;
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito R., Sakai K., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami Y., Takahashi F., Tanaka T.,
RA Tejima T., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M. Hayashizaki Y.;
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RP [6]
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RX MEDLINE=22382257; PubMed=12477932;
RG Name=Igh-4;
DE Igh-4 protein.
DR EMBL; AK007918; BAB25349.1; -.
DR PIR; PH1165; PH1165.
DR PIR; S19966; S19966.
DR PIR; S26746; S26746.
DR HSSP; P01864; 1BQG.
DR MGD; MGI:96443; Igh-1a.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE   473 AA;   51699 MW; 9DED57A514475FBB CRC64;
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0005771; C:multivesicular body; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0001788; F:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0001948; P:antigen processing, classical pathway; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0008333; P:endosome to lysosome transport; IDA.
DR GO; GO:0006910; P:phagocytosis, engulfment; IDA.
DR GO; GO:0006911; P:phagocytosis, recognition; IDA.
DR GO; GO:0050871; P:positive regulation of B-cell activation; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type IIa hypersensit. '; IDA.
DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; IDA.

Matches 113; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

Qy   1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVXMSCKASGYTLTSYNMHWVKQTP 60
         ||||||: :| :: | ||||:||||:|||||||| .||||||:|||||||||:||| |||
Db   1 MEWSWVFLFLLSVTAGVHCQVQLKQSGAELVKPGASVKISCKASGYTFTDYINWVKQRP 60

Qy   61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
         ||||||||||:| ||: |||||||||||||||||||:||| |||:|||||||:|||| ||
Db   61 GQGLEWIGKIGFGSGSTYYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGY 120

Qy 121 E-GALDYWGQGTSVTVSSAKTPPPVYPLVP 150
         : ||||:||||| |||||:|||||:||: |
Db 121 DYDWFAYWGQGTLVTVSAAKTTAPSVYPLAP 151

ID Q99LC4   PRELIMINARY;   PRT;   463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Name=Igh-4;
DE Igh-4 protein.
GN Name=Igh-4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RL "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR PIR; B45837; B45837.
DR HSSP; P01869; 1CL7.
DR MGD; MGI:96446; Igh-4.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR GO; GO:0006955; P:defense response to pathogenic bacteria; IDA.
DR GO; GO:0042830; P:defense response to pathogenic bacteria; IDA.
DR GO; GO:0006911; P:phagocytosis, recognition; IDA.
DR GO; GO:0006910; P:phagocytosis, engulfment; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0019733; F:antibacterial humoral response (sensu Verte.. '; IDA.
DR GO; GO:0001788; F:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type IIa hypersensit. '; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE   463 AA;   51007 MW; EAA674C6BBC30783 CRC64;

Query Match   Best Local Similarity   71.2%;   Score 581;   DB 2;   Length 463;
70.8%;   Pred. No. 1.2e-44;

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 6, 2004, 13:29:00 ; Search time 15.4027 seconds
(without alignments)
955.753 Million cell updates/sec

Title: US-08-836-455-4
Perfect score: 816
Sequence: 1 MECSWVFLFLLSITTGVHSQ.............TVSSAKTTPPPVYPLVPGSL 153
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Databases :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	568	69.6	475	2	S01321	Ig gamma-2b chain
2	563	69.0	469	2	S37483	Ig gamma-2a chain
3	560	68.6	474	1	G2MS11	Ig gamma-2b chain
4	549	67.3	139	2	PS0024	Ig heavy chain pre
5	548.5	67.2	151	2	PL0011	Ig heavy chain pre
6	547	67.0	246	2	PN0444	Ig heavy chain v r
7	537.5	65.9	246	2	S38950	Ig gamma chain - m
8	537.5	65.9	446	2	S40295	Ig gamma chain - m
9	533	65.3	178	2	S29594	Ig gamma chain (WM
10	529	64.8	137	2	H32513	Ig heavy chain pre
11	527.5	64.6	140	2	PH1482	Ig heavy chain v r
12	523.5	64.2	140	1	HVMSG7	Ig heavy chain pre
13	523.5	64.2	166	2	PL0012	Ig heavy chain pre
14	516.5	63.3	140	2	PH1489	Ig heavy chain v r
15	512	62.7	141	2	A39276	Ig heavy chain pre
16	510.5	62.6	138	2	E32513	Ig heavy chain pre
17	507.5	62.2	138	2	S21810	Ig heavy chain pre
18	507	62.1	133	2	PC1155	Ig heavy chain pre
19	506.5	62.1	140	2	PH1488	Ig heavy chain v r
20	502.5	61.6	135	2	PH1493	Ig heavy chain v r
21	502.5	61.6	140	2	PH1498	Ig heavy chain v r
22	502.5	61.6	140	2	PH1484	Ig heavy chain v r
23	501.5	61.5	135	2	PH1494	Ig heavy chain v r
24	501.5	61.5	135	2	PS0057	Ig heavy chain pre
25	499	61.2	139	2	A27609	Ig heavy chain pre
26	497	60.9	139	2	PH1492	Ig heavy chain v r
27	496.5	60.8	135	2	PH1499	Ig heavy chain v r
28	495	60.7	140	2	A30577	Ig heavy chain pre
29	494.5	60.6	140	2	PH1486	Ig heavy chain v r
29	493	60.4	139	1	MHMS18	Ig heavy chain pre
30	491.5	60.2	136	2	PL0208	Ig heavy chain pre
31	491.5	60.2	140	2	A36194	Ig heavy chain v r
32	490	60.0	141	2	JL0076	Ig heavy chain pre
33	487.5	59.7	140	2	PH1483	Ig heavy chain v r
34	484.5	59.4	140	2	T01407	Ig heavy chain (my
35	480	58.8	214	2	PC4202	monoclonal antibod
36	479.5	58.8	140	2	S04575	Ig heavy chain pre
37	476	58.3	171	2	S23623	Ig heavy chain v r
38	472.5	57.9	136	2	S04576	Ig heavy chain pre
39	472	57.8	137	2	P29380	Ig heavy chain pre
40	470.5	57.7	140	2	PH1499	Ig heavy chain v r
41	470	57.6	117	2	S03289	Ig heavy chain pre
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43	470	57.6	137	1	G2MS43	Ig heavy chain pre
44	468	57.4	137	2	E29380	Ig heavy chain pre
45	467.5	57.3	121	2	A26405	Ig heavy chain v r

ALIGNMENTS

RESULT 1
S01321
Ig gamma-2b chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01321
R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
R;ide Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01321
A;Molecule type: mRNA
A;Residues: 1-475 <DE1>
A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F;159-223/Domain: immunoglobulin homology <IMM>

Query Match 69.6%; Score 568; DB 2; Length 475;
Best Local Similarity 71.2%; Pred. No. 1e-37;
Matches 109; Conservative 14; Mismatches 28; Indels 2; Gaps 1;

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Qy    1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
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Db    1 MEWIWIFLFILSGTAGVQSQVQLQQSGAELARPGASVKLSCKASGYTLTSYGISWVKQRT 60

Qy   61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQLSSLTSEDSAVYFCARGNW 120
          |||||||| |||| :|:| |||:|||| :|||||||||||:|:||||||||||||  ||
Db   61 GQGLEWIGEIYPGSGNSYFNEKFKGKRATLTVDKSSSTAYLHLSSLTSEDSAVYFCAGPRQ 120

Qy  121 EGAL--DYWGQGTSVTVSSAKTTPPPVYPLPVLPG 151
          |||   :|||||| ||||||||||||||||||
Db  121 VGLLPFGYWGQGTLVTASAKTTPPSVYPLAPG 153
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RESULT 2
S37483
Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37483
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-469 <DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253

C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM>

Qy   Query Match
      Best Local Similarity   69.0%;   Score 563; DB 2; Length 469;
      Matches 109; Conservative 15; Mismatches 26; Indels 2; Gaps 1;

Qy   1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
         |||||| |||| :| ||| : | |||| **||||||| |||||||| *| * *|||**|
Db   1 MGWSWIFLFLLSGTAGVHCQIQLQQSGPELVKPGASVKISCKASGYTFTDYYINWVKQKP 60

Qy   61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR--G 118
         ||||| || :| : |||||||||||| || |||||||||:|||||||| **||| : G
Db   61 GQGLKWIGWIYPASGNTKYNENFKGKATLTVDTSSSTAYMQLSSLTSEDTAVYFCARAMG 120

Qy 119 NWEGALDYWGQGTSVTVSSAKTTPPVVYPLVP 150
         : |||||||||||| ||||||||| *|||| ||
Db 121 AFATLLDYWGQGTTLTVSSAKTTAPSVYPLAP 152

RESULT 3
G2MS11
Ig gamma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence revision 01-Dec-2000 #text change 09-Jul-2004
A;Accession: S25057; A02157; A26235; A26232; A26233; A53598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m
A;Reference number: S25057
A;Accession: S25057
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <FIS>
A;Cross-references: UNIPROT:P01866; EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from r
A;Reference number: A02157; MUID:80120716; PMID:6766534
A;Contents: a allele
A;Accession: A02157
A;Molecule type: DNA
A;Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A;Cross-references: GB:J00461
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A;Note: the sequence was determined from the germline gene
A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglo
A;Reference number: A26232; MUID:80081502; PMID:117549
A;Accession: A26232
A;Molecule type: DNA
A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU1>
A;Contents: a allele
A;Accession: A26235
A;Reference number: MPC 11
A;Cross-references: A26235; MUID:80081501; PMID:117548
A;Reference number: A26235
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>
A;Accession: A26233
A;Contents: b allele
A;Molecule type: DNA
A;Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
R;Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm
A;Molecule type: DNA
A;Note: Lys-474 is probably removed posttranslationally
A;Residues: 138-161, 'L', 163-189, 'FP', 193-376, 'T', 378-474 <TU1>
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash
J. Biol. Chem. 269, 12345-12350, 1994

A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359; PMID:7512967
A;Accession: A53598
A;Molecule type: protein
A;Status: preliminary
A;Residues: 234-251 <KIM>
C;Genetics:
A;Introns: 138/1; 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F;157-222/Domain: immunoglobulin homology <IM1>
F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: intrachain
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Qy   Query Match
      Best Local Similarity   68.6%;   Score 560; DB 1; Length 474;
      Matches 109; Conservative 13; Mismatches 26; Indels 6; Gaps 2;

Qy   1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
         || |||||||| :| ||| : | |||||||** |||||||||||||| *| *|||||*|
Db   1 MEWSWIFLFLLSGTAGVHSEVQLQQSGAELVNPGASVKMSCKASGYTFITYMHWVKQRP 60

Qy   61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG-- 118
         |||||||| :|:: | |:*||||| || | ||* ||||:*|||||||||| |||
Db   61 GQGLEWIGYINPNKDGTKFNEKFKGKATLTSDKSSNTAYMELSSLTSEDSAVYYCARDYD 120

Qy 119 -NWEGALDYWGQGTSVTVSSAKTTPPVVYPLVPG 151
          : ||||||||| *|| |||||| *||| ||*G
Db 121 YDW---FAYWGQGTLVTVSAAKTTPSVYPLAPG 151

RESULT 4
PS0024
Ig heavy chain precursor V region (6A4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
A;Accession: PS0024
C;Superfamily: immunoglobulin; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
C;Comment: This chain is obtained from an IgG2a monoclonal antibody against Pseudomonas
A;Experimental source: strain BALB/c
A;Molecule type: mRNA
A;Residues: 1-139 <MAR>
A;Accession: PS0024
A;Reference number: PS0023; MUID:89232725; PMID:3149944
A;Title: Cloning and characterization of cDNAs coding for the heavy and light chains of
Gene 74, 335-345, 1988
R;Marget, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Dondey, H.
F;20-139/Domain: immunoglobulin V region #status predicted <IGV>
F;1-19/Domain: signal sequence #status predicted <SIG>
C;Keywords: signal sequence
F;34-117/Domain: immunoglobulin homology <IMM>
F;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

Qy   Query Match
      Best Local Similarity   67.3%;   Score 549; DB 2; Length 139;
      Matches 106; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

Qy   1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
         || |||||| * :| ||||*|*|||||||| |||||||||||||||| *| *|||||*|
Db   1 MERHWIFLFSVTAGVHSQVQLQQSGAELAKPGASVKMSCKASGYTFTAYWMHWVKQRP 60

Qy   61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQLSSLTSEDSAVYCTRSYY 120
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Db   61 GQGLEWIGYINPNTGYTEYNQNFKDKATLTADKSSSTAYMQLSSLTSEDSAVYCTRSYY 120

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: December 6, 2004, 13:38:54 ; Search time 66.8862 seconds
(without alignments)
4898.976 Million cell updates/sec

Title: US-08-836-455-3
Perfect score: 461
Sequence: 1 ATGGAATGCAGCTGGGTCTT.............CTGGTCCCTGGAAGCTTGGG 461
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	461	100.0	461	3	US-09-096-244-3	Sequence 3, Appli
2	324.6	70.4	453	4	US-08-513-968-33	Sequence 33, Appl
3	322	69.8	459	4	US-09-724-138-43	Sequence 43, Appl
4	320	69.4	1683	3	US-09-192-545-1	Sequence 1, Appl
5	311.6	67.6	1570	2	US-08-116-247-6	Sequence 6, Appli
6	311.6	67.6	1570	4	US-09-348-224-6	Sequence 6, Appli
7	310	67.2	1570	4	US-08-303-569B-6	Sequence 6, Appli
8	310	67.2	1570	4	US-09-795-515-6	Sequence 6, Appli
9	304.4	66.0	1572	1	US-08-353-400-23	Sequence 23, Appl
10	299.8	65.0	421	4	US-09-254-180C-142	Sequence 142, App
11	297.2	64.5	9209	4	US-08-149-099C-3	Sequence 3, Appl
12	297.2	64.5	9209	1	US-08-476-275-2	Sequence 2, Appl
13	297.2	64.5	9209	3	US-08-478-967A-3	Sequence 3, Appl
14	297.2	64.5	9209	3	US-08-475-813-3	Sequence 3, Appl
15	297.2	64.5	9209	4	US-08-475-815B-3	Sequence 3, Appl
16	297.2	64.5	18986	2	US-08-819-866-2	Sequence 2, Appl
17	297.2	64.5	18986	2	US-09-023-715-2	Sequence 2, Appli
18	297.2	64.5	18986	4	US-09-343-485A-2	Sequence 2, Appl
19	297	64.5	10844	3	US-08-444-644-41	Sequence 41, Appl
20	297	64.4	10844	3	US-08-444-644A-41	Sequence 41, Appl
21	295.8	64.2	408	5	PCT-US93-11611-3	Sequence 3, Appli
22	295.4	64.1	10785	3	US-08-232-246A-41	Sequence 41, Appl
23	295.4	64.1	10785	3	US-08-232-246A-27	Sequence 27, Appl
24	295.4	64.1	10785	3	US-08-444-644-18	Sequence 18, Appl
25	295.4	64.1	11528	3	US-08-232-246A-18	Sequence 18, Appl
26	294.2	63.8	417	2	US-08-452-164A-7	Sequence 7, Appli
27	293.2	63.6	416	1	US-08-253-877C-7	Sequence 7, Appli
28	293.2	63.6	416	3	US-08-603-024-1	Sequence 1, Appli
29	293.2	63.6	416	4	US-08-450-809-1	Sequence 1, Appli
30	291	63.1	411	2	US-08-574-699A-3	Sequence 3, Appli
31	289.6	62.8	422	1	US-08-482-882-77	Sequence 77, Appli
32	289.6	62.8	422	1	US-08-483-389-77	Sequence 77, Appli
33	289.6	62.8	422	2	US-08-487-1133D-77	Sequence 77, Appl
34	289.6	62.8	422	2	US-08-473-503-77	Sequence 77, Appli
35	289.6	62.8	422	2	US-08-483-932-77	Sequence 77, Appl
36	289.6	62.8	422	2	US-08-720-420A-77	Sequence 77, Appl
37	289.6	62.8	422	3	US-08-714-017-77	Sequence 77, Appl
38	289.6	62.8	422	3	US-08-475-680-77	Sequence 77, Appl
39	288.4	62.6	1425	4	US-09-592-998C-6	Sequence 6, Appli
40	288.4	62.6	690	2	US-08-634-783A-1	Sequence 1, Appli
41	288.4	62.6	690	3	US-09-070-817-1	Sequence 1, Appli
42	286.6	62.2	405	4	US-07-634-278-68	Sequence 68, Appl
43	286.6	62.2	405	1	US-08-477-728-68	Sequence 68, Appl
44	286.6	62.2	405	1	US-08-474-040-68	Sequence 68, Appl
45	286.6	62.2	405	1	US-08-487-200-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1
US-09-096-244-3
; Sequence 3, Application US/09096244
; Patent No. 6274143
; GENERAL INFORMATION:
;   APPLICANT: Chatterjee, Malaya
;   APPLICANT: Foon, Kenneth A.
;   TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
;   TITLE OF INVENTION: HMFG-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 11D10
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MORRISON & FOERSTER
;   STREET: 755 PAGE MILL ROAD
;   CITY: PALO ALTO
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304-1018
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/096,244
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Polizzi, Catherine M.
;   REGISTRATION NUMBER: 40,130
;   REFERENCE/DOCKET NUMBER: 30414-20006.00
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 813-5600
;   TELEFAX: (650) 494-0792
;   TELEX: 706141
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 461 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..459
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: 58
US-09-096-244-3

Query Match   100.0%; Score 461; DB 3; Length 461;

Best Local Similarity   100.0%;   Pred. No. 7.4e-134;
Matches 461; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGGAAATGCAGCTGGGTCTTTCTTCTTCCTTCCTTCGTCAATAACTACAGGTGTCCACTCCCAG 60
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Db   1 ATGGAAATGCAGCTGGGTCTTTCTTCTTCCTTCCTTCGTCAATAACTACAGGTGTCCACTCCCAG 60

Qy   61 GCTTATCTACAGCAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCTTATCTACAGCAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCC 120

Qy   121 TGCAAGGCTTCTGGCTACACAATTGACCAGTTACACTGGGTAAAGCAGACACACCT 180
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Db   121 TGCAAGGCTTCTGGCTACACAATTGACCAGTTACACTGGGTAAAGCAGACACACCT 180

Qy   181 GGACAGGGGCCTGGAATGGATTGGAAATATTTTTCCTGGAAATGGGTGATACTTACTTACACAAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGACAGGGGCCTGGAATGGATTGGAAATATTTTTCCTGGAAATGGGTGATACTTACTTACACAAT 240

Qy   241 CAGAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACACAGCCTACATG 300
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Db   241 CAGAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACACAGCCTACATG 300

Qy   301 CAGATCAGCAGCCTGACATCTGCGGTCTATTTCTGTGCAAGAGAGGGAACTGG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CAGATCAGCAGCCTGACATCTGCGGTCTATTTCTGTGCAAGAGAGGGAACTGG 360

Qy   361 GAGGGTGCTCTGGACTACTGGGGTCAAGAGAACCCTCAGTCACCGTCTCCTCAGCCAAAACG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAGGGTGCTCTGGACTACTGGGGTCAAGAGAACCCTCAGTCACCGTCTCCTCAGCCAAAACG 420

Qy   421 ACACCCCCACCCGTCTATCCACTGGTCCCTGGGAAGCTTGGG 461
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Db   421 ACACCCCCACCCGTCTATCCACTGGTCCCTGGGAAGCTTGGG 461

RESULT 2
US-08-513-968-33
; Sequence 33, Application US/08513968
; Patent No. 6114143
GENERAL INFORMATION:

APPLICANT: EDA, Yasuyuki
APPLICANT: MAEDA, Hiroaki
APPLICANT: MAKIZUMI, Keiichi
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: OSATOMI, Kiyoshi
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: HIGUCHI, Hirofumi
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
  ADDRESSEE: BROWDY AND NEIMARK
  STREET: 419 Seventh Street, N.W., Suite 300
  CITY: Washington
  STATE: D.C.
  COUNTRY: USA
  ZIP: 20004
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/513,968
  FILING DATE: 11-SEP-1995
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: JP 78913/1993
  FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
  NAME: BROWDY, Roger L.
  REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: EDA-1
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 202-628-5197
  TELEFAX: 202-737-3528
  TELEX: 248633
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
  LENGTH: 453 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
  NAME/KEY: CDS
  LOCATION: 1..453
US-08-513-968-33

Query Match   70.4%;   Score 324.6; DB 3;   Length 453;
Best Local Similarity 83.3%;   Pred. No. 2.2e-91;
Matches 369; Conservative   0; Mismatches 74; Indels   0; Gaps   0;

Qy   1 ATGGAAATGCAGCTGGGTCTCTTTCTTCTTCCTTCCTTCGTCAATAACTACAGGTGTCCACTCCCAG 60
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Db   1 ATGGAAATGGAGCTGGGTCTTTTATCTTTCTCCCTGTCAATAACTACAGGTGTCCACTCCCAG 60

Qy   61 GCTTATCTACAGCAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCC 120
          ||||||||| |||||||||||| || ||||||||||||||| ||||||||||||||||
Db   61 GTCCAGCTGCAGCAGTCTGGAGCTGAGCTGGTGGGGCCTGGGGCTTCAGTGAAGATGTTC 120

Qy   121 TGCAAGGCTTCTGGCTACACAATTGACCAGTTACACTGGGTAAAGCAGACACACCT 180
          |||||||||||||| ||||||||||||||| |||||||| ||||||||||||||
Db   121 TGCAAGGCTTCTGGATACACATTCACTAACTCCTGGATAGGTTGGGTTAGGCAGAGGCCT 180

Qy   181 GGACAGGGGCCTGGAATGGATTGGAAATATTTTTCCTGGAAATGGGTGATACTTACTTACACAAT 240
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Db   181 GGACATGGCCTTGAGTGGATTGGAGAGATTTTACCTGGAAGTGGTGATACTAACTACAAT 240

Qy   241 CAGAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACACAGCCTACATG 300
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Db   241 GAGATCTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTATATG 300

Qy   301 CAGATCAGCAGCCTGACATCTGCGGTCTATTTCTGTGCAAGAGAGGGAACTGG 360
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Db   301 CAGCTCAGCAGCCTGACATCTGAGGACTCTGCCATCTATTACTGTGCAAGGGGATACCG 360

Qy   361 GAGGGTGCTCTGGACTACTGGGGTCAAGAGAACCCTCAGTCACCGTCTCCTCAGCCAAAACG 420
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Db   361 GGATATCCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACA 420

Qy   421 ACACCCCCACCCGTCTATCCACTGGTCCCTGGGAAGCTTGGG 461
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Db   421 ACAGCCCCATCCGTCTATCCACTGGCCCT 461

RESULT 3
US-09-724-138-43
; Sequence 43, Application US/09724138
; Patent No. 6652852
GENERAL INFORMATION:

APPLICANT: Robinson, Randy
APPLICANT: Liu, Alvin
APPLICANT: Ledbetter, Jeffrey
TITLE OF INVENTION: Chimeric Antibody with Specificity to Human B Cell Surface Anti
FILE REFERENCE: PPI-001CN2
CURRENT APPLICATION NUMBER: US/09/724,138
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/630198
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 09/021934
PRIOR FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: US 08/471984
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 07/665939

RESULT 3
US-09-724-138-43
; Sequence 43, Application US/09724138
; Patent No. 6652852
GENERAL INFORMATION:

Best Local Similarity ...; Conservative   0; Mismatches ...; Indels   0; Gaps   0;

Qy   1 ATGGAAATGCAGCTGGGTCTCTTTCTTCTTCCTTCCTTCGTCAATAACTACAGGTGTCCACTCCCAG 60
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Qy   61 GCTTATCTACAGCAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCC 120
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Qy   121 TGCAAGGCTTCTGGCTACACAATTGACCAGTTACACTGGGTAAAGCAGACACACCT 180
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Db   121 TGCAAGGCTTCTGGATACACATTCACTAACTCCTGGATAGGTTGGGTTAGGCAGAGGCCT 180

Qy   181 GGACAGGGGCCTGGAATGGATTGGAAATATTTTTCCTGGAAATGGGTGATACTTACTTACACAAT 240
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Db   181 GGACATGGCCTTGAGTGGATTGGAGAGATTTTACCTGGAAGTGGTGATACTAACTACAAT 240

Qy   241 CAGAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACACAGCCTACATG 300
          ||||| || |||||||| ||| |||| |||||| |||| ||||| ||| ||||||
Db   241 GAGATCTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTATATG 300

Qy   301 CAGATCAGCAGCCTGACATCTGCGGTCTATTTCTGTGCAAGAGAGGGAACTGG 360
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Db   301 CAGCTCAGCAGCCTGACATCTGAGGACTCTGCCATCTATTACTGTGCAAGAGGGATACCG 360

Qy   361 GAGGGTGCTCTGGACTACTGGGGTCAAGAGAACCCTCAGTCACCGTCTCCTCAGCCAAAACG 420
          |||| || |||||||||||||| |||| ||| ||| |||||| |||| || ||||
Db   361 GGATATCCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACA 420

Qy   421 ACACCCCCACCCGTCTATCCACTCACT 443
          || |||||||||||||| |||||
Db   421 ACAGCCCCATCCGTCTATGCACT 443

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 13:36:24 ; Search time 352.953 Seconds
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6856.387 Million cell updates/sec

Title: US-08-836-455-3
Perfect score: 461
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4134886 seqs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
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11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	461	100.0	461	2	AAT85150	AAT85150 Murine mo
2	461	100.0	461	2	AAV83773	AAV83773 Antibody
3	461	100.0	461	8	AAL51274	AAL51274 Mouse 11D
4	337.6	73.2	1401	2	AAd58178	AAd58178 Mouse vir
5	327.2	71.0	409	3	AAZ87715	AAZ87715 Anti-huma
6	327.2	71.0	409	4	AAF70192	AAF70192 Anti-huma
7	326.6	70.8	736	2	ABx16571	ABx16571 Mouse DNA
8	323	70.1	540	1	AAN91645	AAN91645 Heavy cha
9	322	69.8	458	1	AAN91146	AAN91146 2H7 Vh se
10	322	69.8	459	4	AAV82357	AAV82357 Mouse ant
11	322	69.8	459	4	AAH22070	AAH22070 2H7 heavy
12	322	69.8	459	10	ADc65026	ADc65026 Immunoglo
13	322	69.8	491	2	AAt70868	AAt70868 2H7 heavy
14	322	69.8	491	2	AAV03926	AAV03926 Mouse 2H7
15	322	69.8	491	2	AAV18557	AAV18557 Mouse 2H7
16	322	69.8	491	2	AAV18593	AAV18593 Mouse 2H7
17	322	69.8	518	2	AAT36316	AAT36316 2H7 antib
18	322	69.5	520	2	AAt51042	AAt51042 Coding se
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21	314.8	68.3	494	2	AAV20085	AAV20085 Consensus

ALIGNMENTS

22	311.6	67.6	1570	2	AAQ12637	AAq12637 Monoclona
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25	309.4	67.1	459	1	AAN70971	AAn70971 2H7 VH se
26	308.6	66.9	420	4	AAF81910	AAf81910 Anti-CA12
27	308.2	66.9	588	2	AAQ43385	AAq43385 H-chain V
28	308.2	66.9	1392	2	AAT62936	AAt62936 3F4 (Chim
29	308.2	66.9	1395	2	AAT62935	AAt62935 Murine an
30	308.2	66.9	3400	2	AAT62937	AAt62937 3F4, human
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32	306.4	66.5	468	3	AAV05544	AAv05544 Mouse sec
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36	299	64.9	458	2	AAQ15164	AAq15164 Nucleotid
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38	297.4	64.5	1773	2	AAV66735	AAv66735 Anti-huma
39	297.4	64.5	1773	3	AAA78202	AAa78202 Anti-huma
40	297.2	64.5	1083	6	AAD45753	AAd45753 Human CH2
41	297.2	64.5	1083	3	ABZ24017	ABz24017 Antibody
42	297.2	64.5	1413	3	AAA63531	AAa63531 DNA encod
43	297.2	64.5	1413	6	AAD45752	AAd45752 Human C2B
44	297.2	64.5	1413	8	ABZ24016	ABz24016 Antibody
45	297.2	64.5	9208	2	AAQ65629	AAq65629 Vector co

RESULT 1
ID AAT85150
AAT85150 standard; cDNA; 461 BP.
XX
AC AAT85150;
XX
DT 25-MAR-2003 (revised)
DT 04-JAN-1998 (first entry)
XX
DE Murine monoclonal anti-idiotype antibody 11D10 VH cDNA.
XX
KW Monoclonal antibody; 11D10; anti-idiotype antibody; mucin;
KW human milk fat globule; HMFG; tumour; breast cancer; vaccine; ss.
XX
OS Mus musculus.
XX
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FT mat_peptide   58..461
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PN WO9726699-A2.
XX
PD 26-JUN-1997.
XX
PF 19-DEC-1996; 96WO-US020757.
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PR 20-DEC-1995; 95US-00575762.
PR 26-JAN-1996; 96US-00591965.
PR 13-DEC-1996; 96US-00766350.
XX
PA (KENT) UNIV KENTUCKY.
XX
PI Chatterjee M, Foon KA, Chatterjee SK;
XX
DR WPI; 1997-341690/31.
DR P-PSDB; AAW27120.
XX
PT Monoclonal anti-idiotype antibody 11D10 - elicits immune response against
PT human milk fat globule disease associated tumours, especially breast
PT cancer.
XX
PS Claim 12; Page 94; 130pp; English.

XX
CC   This cDNA sequence encodes the heavy chain variable region VH (AAW85150)
CC   of monoclonal anti-idiotype antibody 11D10 produced by hybridoma cell
CC   line ATCC 12020. 11D10 was obtained by immunising naive mice with MC-10
CC   anti-HMFG antibody to obtain an anti-idiotype response. It elicits an
CC   immune response against a specific epitope of a high mol.wt. mucin of
CC   human milk fat globule (HMFG). It induces an immunological response to
CC   HMFG in mice, rabbits, monkeys and patients with advanced HMFG-associated
CC   tumours. Pharmaceutical compositions and vaccines comprising 11D10,
CC   polypeptides and/or 11D10 polynucleotides are claimed. Also claimed are
CC   diagnostic kits and methods of using 11D10, 11D10 polypeptides and/or
CC   11D10 polynucleotides, including methods of treating HMFG- associated
CC   tumours. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 461 BP; 112 A; 121 C; 119 G; 109 T; 0 U; 0 Other;

Query Match   100.0%; Score 461; DB 2; Length 461;
Best Local Similarity   100.0%;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   61 GCTTATCTACAGCAGTCGTCTGGGGCCTCAGCGTCGTGAGGTCTCAGTGAAGATGTCC 120
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Db   61 GCTTATCTACAGCAGTCGTCTGGGGCCTCAGCGTCGTGAGGTCTCAGTGAAGATGTCC 120

Qy   121 TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGGCACTGGGTAAAGCAGACACCT 180
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Qy   181 GGACAGGGCCTGGAATGGAATTGGAAATATTTTCCTGGAAATGGTGATACTTACTACAAT 240
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Db   421 ACACCCCCACCCGTCTATCCACTGGTCCCTGGAAGCTTGGG 461

RESULT 2
AAV83773
ID   AAV83773 standard; cDNA; 461 BP.
XX
AC   AAV83773;
XX
DT   16-MAR-1999 (first entry)
XX
DE   Antibody 11D10 heavy chain variable region coding sequence.
XX
KW   Antibody 11D10 heavy chain variable region coding sequence.
KW   Murine; mouse; antibody; light chain; variable region; anti-idiotype; ss;
KW   human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
OS   Mus sp.
XX

Key   Location/Qualifiers
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FT   mat_peptide   58..459
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PN   WO9856419-A1.
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PD   17-DEC-1998.
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PF   12-JUN-1998;   98WO-US012250.
XX
PR   13-JUN-1997;   97US-0049540P.
PR   11-JUN-1998;   98US-00096244.
XX
PI   (KENT) UNIV KENTUCKY RES FOUND.
XX
PA   Chatterjee M, Foon KA;
XX
PT   WPI; 1999-060029/05.
DR   P-PSDB; AAW87594.
XX
PS   Disclosure; Fig 2; 54pp; English.
XX
CC   This sequence represents the coding sequence for the murine antibody
CC   11D10 heavy chain variable region. This anti-idiotype antibody is used to
CC   delay the development of, or treat, a human milk fat globule (HMFG)
CC   associated tumour in an individual having low tumour burden. The antibody
CC   11D10 is used to prevent the recurrence of HMFG-associated tumours e.g.
CC   ovarian, non-small cell lung and pancreatic carcinoma, especially for
CC   treating breast tumours
XX
SQ   Sequence 461 BP; 112 A; 121 C; 119 G; 109 T; 0 U; 0 Other;

Delaying development of, or treating, HMFG-associated tumours - using
anti-idiotype antibody 11D10 raised against antibodies to human milk fat
globule protein.

Query Match   100.0%; Score 461; DB 2; Length 461;
Best Local Similarity   100.0%;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGGAATGCAGCTGGGTCTTTCTCTTCCTCCTGTCAATAACTACACAGGTGTCCACTCCCAG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGAATGCAGCTGGGTCTTTCTCTTCCTCCTGTCAATAACTACACAGGTGTCCACTCCCAG 60

Qy   61 GCTTATCTACAGCAGTCGTCTGGGGCCTCAGCGTCGTGAGGTCTCAGTGAAGATGTCC 120
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Qy   121 TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGGCACTGGGTAAAGCAGACACCT 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGGCACTGGGTAAAGCAGACACCT 180

Qy   181 GGACAGGGCCTGGAATGGAATTGGAAATATTTTCCTGGAAATGGTGATACTTACTACAAT 240
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Db   181 GGACAGGGCCTGGAATGGAATTGGAAATATTTTCCTGGAAATGGTGATACTTACTACAAT 240

Qy   241 CAGAAGTTTAAGGGCAAGGCCCTCAGTTGACTGACTGCAGACACATCCTCCAGCACAGCCTACATG 300
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Qy   301 GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACG 360
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Qy   421 ACACCCCCACCCGTCTATCCACTGGTCCCTGGAAGCTTGGG 461
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OM nucleic - nucleic search, using sw model

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                                         GenCore version 5.1.6
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Run on:               December 6, 2004, 13:39:34 ; Search time 2427.45 Seconds
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Title:          US-08-836-455-3
Perfect score:  461
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Scoring table:  IDENTITY_NUC
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Searched:       4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters:  9053458

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB ID	Description
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4	355.2	77.0	471	10	AB050080	AB050080 Mus muscu
5	353.6	76.7	457	10	AY178830	AY178830 Mus muscu
6	337.8	73.3	1542	10	BC002121	BC002121 Mus muscu
7	328.2	71.2	483	10	MMU39899	U39899 Mus musculu
8	327.2	71.0	409	6	BD092129	BD092129 Diagnosti
9	325	70.5	1544	10	MUSIGB1H1	D14625 Mus musculu
10	324.6	70.4	453	6	AR109947	AR109947 Sequence
11	323	70.1	453	6	MUSIGHALPA	M28834 Mus musculu
12	323	70.1	540	6	A13735	A13735 variable re
13	322	69.8	458	6	I05921	I05921 Sequence 37
14	322	69.8	458	6	I08811	I08811 Sequence 12
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19	320.6	69.5	1553	6	E08434	E08434 cDNA encodi

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20  320.2  69.5   902   12  XXU49832   U49832 Synthetic s
21  320    69.4  1683    6  E35543     E35543 Transgenic
22  318.6  69.1   473   10  AB050071   AB050071 Mus muscu
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25  312.6  67.8   534   10  AY621090   AY621090 Mus muscu
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27  311.6  67.6  1570    6  A22261     A22261 M.musculus
28  311.6  67.6  1570    6  A77138     A77138 Sequence 6
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30  310.6  67.4  1526   10  MMU55622   AJ555622 Mus muscu
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40  308    66.6   490   10  AF466769   AF466769 Mus muscu
41  307    66.6  1558   10  MUSIGH4C11 M54977 Mus musculu
42  306.8  66.6   484   10  MMU416332  MMU416332 Mus muscu
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ALIGNMENTS

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ACCESSION   AR164506
VERSION     AR164506.1  GI:16237556
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 461)
  AUTHORS   Chatterjee,M. and Foon,K.A.
  TITLE     Methods of delaying development of HMFG-associated tumors using
            anti-idiotype antibody 11D10
  JOURNAL   Patent: US 6274143-A 3 14-AUG-2001;
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Query Match   100.0%; Score 461; DB 6; Length 461;
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Matches 461; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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RESULT 2

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DEFINITION   Methods of delaying development of HMFG-associated tumors using
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ACCESSION   BD085738
VERSION   BD085738.1 GI:22631348
KEYWORDS   JP 2001523269-A/2.
SOURCE   unidentified
  ORGANISM   unidentified
             unclassified.
REFERENCE   1 (bases 1 to 461)
  AUTHORS   Chatterjee,M. and Foon,K.A.
  TITLE   Methods of delaying development of HMFG-associated tumors using
             anti-idiotype antibody 11D10
  JOURNAL   Patent: JP 2001523269-A 2 20-NOV-2001;
             THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
COMMENT   OS Unidentified
             PN JP 2001523269-A/2
             PD 20-NOV-2001
             PF 12-JUN-1998 JP 199503252
             PR 13-JUN-1997 US 60/049540,11-JUN-1998 US   09/096244 PI
             PC A61K39/395,A61K39/39//C07K16/42
             PS MALAYA CHATTERJEE, KENNETH A FOON
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             using
             CC anti-idiotype antibody 11D10
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ORIGIN

Query Match   100.0%;   Score 461; DB 6; Length 461;
Best Local Similarity   100.0%; Pred. No. 2.6e-146;
Matches 461; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGAAGTTTAAGGGCAAGGCCACATCCTCAGACACATCCTCCAGCACAGCCTACATG 300

Qy   301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACTGG 360
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Db   361 GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACG 420

Qy   421 ACACCCCCACCCGTCTATCCACTGGGTCCCTGGAAGCTTGGG 461
              ||||||||||||||||||||||||||||||||||||||||||
Db   421 ACACCCCCACCCGTCTATCCACTGGGTCCCTGGAAGCTTGGG 461

RESULT 3

LOCUS   AF124720   411 bp   mRNA   linear   ROD 22-MAY-2001
DEFINITION   Mus musculus immunoglobulin heavy chain mRNA, partial cds.
ACCESSION   AF124720
VERSION   AF124720.1 GI:14164544
KEYWORDS   .
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 411)
  AUTHORS   Tripathi,P.K., Qin,H., Bhattacharya-Chatterjee,M., Ceriani,R.L.,
             Foon,K.A. and Chatterjee,S.K.
  TITLE   Construction and characterization of a chimeric fusion protein
             consisting of an anti-idiotype antibody mimicking a breast
             cancer-associated antigen and the cytokine GM-CSF
  JOURNAL   Hybridoma 18 (2), 193-202 (1999)
  MEDLINE   99306687
  PUBMED   10380019
REFERENCE   2 (bases 1 to 411)
  AUTHORS   Chatterjee,S.K. and Tripathi,P.K.
  TITLE   Direct Submission
  JOURNAL   Submitted (29-JAN-1999) Internal Medicine, University of Kentucky,
             800 Rose Street, Lexington, KY 40536, USA
FEATURES   Location/Qualifiers
     source   1..411
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="BALB/c"
                     /db_xref="taxon:10090"
     CDS   1..>411
                     /codon_start=1
                     /product="immunoglobulin heavy chain"
                     /protein_id="AAK55119.1"
                     /db_xref="GI:14164545"
                     /translation="MKCSWVFLFLLSTTGVHSQAYLQQSGAELVRSGASVKMSCKAS
                     GYTLTSYWMHWVKQTPGQGLEWIGNIFPGNGDTYYNQKFKGKASLTPDTSSSTAYMQI
                     SSLTSEDSAVYFCARGNWEGALDYWGQGTSVVSS"

ORIGIN

Query Match   88.8%;   Score 409.4; DB 10; Length 411;
Best Local Similarity   99.8%; Pred. No. 1.3e-128;
Matches 410; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGAATGCAGCTGGGTCTTTCTCTTCCTGTCAATAACTACAGGTGTTCACTCCCAG 60
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGAAATGCAGCTGGGTCTTTCTCTTCCTTCTCTCCACTACAGGTGTCCACTCCCAG 60

Qy   61 GCTTATCTACAGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCTTATCTACAGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCC 120

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                    GenCore version 5.1.6
             Copyright (c) 1993 - 2004 Compugen Ltd.


OM protein - protein search, using sw model

Run on:          December  6, 2004, 13:29:00 ; Search time 54.9832 seconds
                                             (without alignments)
                                             1517.360 Million cell updates/sec

Title:           US-08-836-455-2
Perfect Score:   740
Sequence:        1 MGAPAQILGFLLLLFPGTRC..........IKRADAAPTVSIPPSSKLG 145

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters:          1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries.

Database :       UniProt.02:*
                 1:    uniprot_sprot:*
                 2:    uniprot_trembl:*


    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.


                              SUMMARIES

Result                   Query
No.     Score   Match Length  DB  ID        Description
------  -----   ------------  --  --------   -----------
  1     642     127        2  Q92SS9     Q92SS9 mus musculu
  2     596     130        1  KV5G_MOUSE P01639 mus musculu
  3     516     236        2  Q7TMK3     Q7tmk3 mus musculu
  4     513     234        2  Q8R062     Q8r062 mus musculu
  5     506     236        2  Q91WF8     Q91wf8 mus musculu
  6     501     236        2  Q7S98      Q7tS98 mus musculu
  7     492     233        2  Q91WS9     Q91ws9 mus musculu
  8     489     236        2  Q6GMX9     Q6gmx9 homo sapien
  9     475     236        2  Q6GMX8     Q6gmx8 homo sapien
 10     471     236        2  Q6GMW1     Q6gmw1 homo sapien
 11     469     236        2  Q7Z3Y4     Q7z3y4 homo sapien
 12     461     236        2  Q6PIH7     Q6pih7 homo sapien
 13     461     236        2  Aah34141   Aah34141 homo sapi
 14     460     236        2  Q7Z473     Q7z473 homo sapien
 15     460     234        2  Q6PKE4     Q6pke4 mus musculu
 16     460     234        2  AAH02112   Aah02112 mus muscu
 17     452     117        1  KV5H_MOUSE P01641 mus musculu
 18     450     234        2  Q8VCP0     Q8vcp0 mus musculu
 19     450     236        2  Q6GMX0     Q6gmx0 homo sapien
 20     442     236        2  Q6PIT5     Q6pit5 homo sapien
 21     442     236        2  AAH29444   Aah29444 homo sapi
 22     433     214        2  Q9R1A5     Q9r1a5 mus musculu
 23     426     236        2  Q6PIH4     Q6pih4 homo sapien
 24     426     236        2  AAH34146   Aah34146 homo sapi
 25     416.5   99         2  AAH11068   Aah11068 mus muscu
 26     416     234        2  AAH30813   Aah30813 homo sapi
 27     412     128        1  KV5E_MOUSE P01637 mus musculu
 28     408     111        2  AAR10992   Aar10992 mus muscu
 29     403     103        2  AAR11025   Aar11025 mus muscu
 30     394     129        1  KV1W_HUMAN P04431 homo sapien
 31     393.5   235        2  Q6GMV9     Q6gmv9 homo sapien
 32     391.5   239        2  Q8K0F8     Q8k0f8 mus musculu
 33     390.5   235        2  Q7TMK0     Q7tmk0 mus musculu
 34     389.5   235        2  Q6GMW0     Q6gmw0 homo sapien
 35     389     108        1  KV5J_MOUSE P01643 mus musculu
 36     384.5   235        2  Q6PJF2     Q6pjf2 homo sapien
 37     384.5   235        2  Aah16380   Aah16380 homo sapi
 38     384     108        1  KV5M_MOUSE P01644 mus musculu
 39     383     108        1  KV5K_MOUSE P01648 mus musculu
 40     382.5   235        2  Q91WI2     Q91wi2 mus musculu
 41     382     108        1  KV5O_MOUSE P01646 mus musculu
 42     382     108        1  KV5N_MOUSE P01648 mus musculu
 43     382     108        1  Q6P5S8     Q6p5s8 homo sapien
 44     382     236        2  AAH62704   Aah62704 homo sapi
 45     381     117        1  KVII_HUMAN P01601 homo sapien
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                              ALIGNMENTS

```
RESULT 1
Q92SS9

ID   Q92SS9;         PRELIMINARY;        PRT;      127 AA.
AC   Q92SS9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunoglobulin light chain (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=99306687; PubMed=10380019;
RA   Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
RA   Foon K.A., Chatterjee S.K.;
RT   "Construction and characterization of a chimeric fusion protein
RT   consisting of an anti-idiotype antibody mimicking a breast cancer-
RT   associated antigen and the cytokine GM-CSF.";
RL   Hybridoma 18:193-202(1999).
DR   EMBL; AF124721; AAK55120.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
NON_TER   127   127
SEQUENCE   127 AA;  13794 MW;  13F61BEBB981FA5 CRC64;

Query Match             86.8%;   Score 642;  DB 2;  Length 127;
Best Local Similarity   99.2%;   Pred. No. 7.4e-55;
Matches  126;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy          1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60

Qy         61 DGTIKRLIYATSSLSGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGTIKRLIYATSSLSGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120

Qy        121 GTKLEIK 127
              |||||||
Db        121 GTKLEIK 127


RESULT 2
KV5G_MOUSE

ID   KV5G_MOUSE      STANDARD;        PRT;      130 AA.
AC   P01639; P01640;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
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RESULT 3
Q7TMK3

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DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-V region MOPC 41 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=79221900; PubMed=111146;
RA   Seidman J.G., Max E.E., Leder P.;
RT   "A kappa-immunoglobulin gene is formed by site-specific recombination
RT   without further somatic mutation.";
RL   Nature 280:370-375(1979).
RN   [2]
RP   SEQUENCE OF 1-33.
RX   MEDLINE=77148916; PubMed=403522;
RA   Burstein Y., Schechter I.;
RT   "Amino acid sequence of the NH2-terminal extra piece segments of the
RT   precursors of mouse immunoglobulin lambdaI-type and kappa-type light
RT   chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
RN   [3]
RP   SEQUENCE OF 23-130.
RX   MEDLINE=67056897; PubMed=4162931;
RA   Gray W.R., Dreyer W.J., Hood L.;
RT   "Mechanism of antibody synthesis: size differences between mouse kappa
RT   chains.";
RL   Science 155:465-467(1967).
CC   -!- MISCELLANEOUS: This precursor was synthesized in a cell-free
CC       system directed by mRNA isolated from myeloma polysomes.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A93211; KVMSM4.
DR   HSSP; P01594; 1JV5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Direct protein sequencing;
KW   Bence-Jones protein; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    130       Ig kappa chain V-V region MOPC 41.
FT   DOMAIN       23    130       Framework-1.
FT   DOMAIN       46     56       Complementarity-determining-1.
FT   DOMAIN       57     71       Framework-2.
FT   DOMAIN       72     78       Complementarity-determining-2.
FT   DOMAIN       79    110       Framework-3.
FT   DOMAIN      111    119       Complementarity-determining-3.
FT   DOMAIN      120    129       Framework-4.
FT   DISULFID     45    110       By similarity.
FT   VARIANT       1      2       Missing (in 25% of the molecules).
FT   NON_TER       1
SQ   SEQUENCE   130 AA;  14311 MW;  5EFE0FE71D5F1BEC CRC64;
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Best Local Similarity   92.2%;
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Qy          1 MGAPAQILGFLLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60
              ||||||:|||||||||:||||||||||||||||||||:::.|||||||:||:.::||||||
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Qy         61 DGTIKRLIYATSSLGSGVPKRFSGSRSGGDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
              |||||||||||||::|||||||||||||:|||||||||||||:|||||||||||||:|||
Db         63 DGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGG 122

Qy        121 GTKLEIKR 128
              ||||||||
Db        123 GTKLEIKR 130
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AC   Q7TMK3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
DR   EMBL; BC055906; AAH55906.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  26299 MW;  0DB03488AAA6396F CRC64;
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Query Match             69.7%;  Score 516;  DB 2;  Length 236;
Best Local Similarity   71.3%;
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              ||||||:||||||||| ||.||||:||||||.|.|||.|||.|||||||||:|:||| ||:|
Db          3 MRAPAQFFGFLLLLLWFPGIRCDIKMTQSPSSMYASLGERVTITCKASQDIKSYLSWYQKP 62

Qy         61 DGTIKRLIYATSSLGSGVPKRFSGSRSGGDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
              |||:|||||||.:|:.||:.||.|||:.:|||.|||||||||.:.:||||:|:..|:||||
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Qy        121 GTKLEIKRADAAPTVSIFPPSSK 143
              |||||||||||||||||||||:
Db        123 GTKLEIKRADAAPTVSIFPPSSE 145
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RESULT 4
Q8R062

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OM protein - protein search, using sw model

Run on: December 6, 2004, 13:29:00 ; Search time 14.573 Seconds
(without alignments)
955.753 Million cell updates/sec

Title: US-08-836-455-2
Perfect score: 740
Sequence: 1 MGAPAQILGFLLLLFPGTRC...........IKRADAAPTVSIFPPSSKLG 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	596	80.5	130	1	KVMSM4	Ig kappa chain pre
2	501	67.7	106	2	PL0260	Ig kappa chain V r
3	497	67.2	106	2	PL0259	Ig kappa chain V r
4	496	67.0	234	2	S14237	Ig kappa chain pre
5	478	64.6	129	2	D32513	Ig kappa chain pre
6	459	62.0	106	2	PL0262	Ig kappa chain V r
7	452	61.1	117	2	KVMS3B	Ig kappa chain V r
8	447	60.4	234	1	S01320	Ig kappa chain pre
9	445	60.1	108	4	B47271	Ig kappa chain pre
10	443	59.9	128	2	A26406	nitrophenyl phosph
11	439	59.3	127	2	PHI224	Ig kappa chain pre
12	438	59.2	129	2	S40369	Ig kappa chain - h
13	435	58.8	98	2	PH1062	Ig light chain V r
14	435	58.8	126	2	A34904	Ig kappa chain pre
15	434	58.6	125	2	S40353	Ig kappa chain V-J
16	434	58.6	130	2	S40368	Ig kappa chain - h
17	433	58.5	129	2	B23986	Ig kappa chain pre
18	431	58.2	129	2	S40380	Ig kappa chain pre
19	429	58.0	141	2	A49134	Ig kappa chain V-I
20	428.5	57.9	230	2	S33161	Ig kappa chain - s
21	428	57.8	127	2	S33317	Ig kappa chain - h
22	426	57.6	127	2	S52447	Ig kappa chain V r
23	425	57.4	132	2	S40334	Ig kappa chain - h
24	424	57.3	115	2	JL0080	Ig kappa chain - h
25	422	57.0	123	2	S40313	Ig kappa chain V-J
26	419	56.6	88	2	PL0261	Ig kappa chain V-J
27	419	56.6	129	2	S52789	Ig kappa chain V-J
28	419	56.6	131	2	S40352	Ig kappa chain V-J
29	418	56.5	125	2	S40349	Ig kappa chain V-J
30	418	56.5	127	2	S40367	Ig kappa chain V-J
31	416	56.2	129	2	S52793	Ig kappa chain V r
32	416	56.1	128	2	S46372	Ig light chain var
33	413	55.8	125	2	S40333	Ig kappa chain V-J
34	412	55.7	128	1	KVMST1	Ig kappa chain pre
35	410	55.4	123	2	S40331	Ig kappa chain - h
36	410	55.3	132	2	S38646	Ig kappa chain V r
37	409	55.3	128	2	PL0101	Ig kappa chain pre
38	407	55.0	101	2	C28840	Ig kappa chain pre
39	407	55.0	101	2	B28840	Ig kappa chain pre
40	405	54.7	125	2	S40316	Ig kappa chain V-J
41	405	54.7	126	2	S40335	Ig kappa chain V-J
42	403.5	54.5	135	2	S24320	Ig kappa chain V-J
43	402	54.3	144	2	S40315	Ig kappa chain - h
44	402	54.1	125	2	PL0106	Ig kappa chain - h
45	400.5	54.1	129	2	S52792	Ig kappa chain V r

ALIGNMENTS

RESULT 1
KVMSM4

Ig kappa chain precursor V region (MOPC 41) - mouse
N;Contains: Ig kappa chain precursor V region VK41
C;Species: Mus musculus (house mouse)
C;Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text change 09-Jul-2004
C;Accession: A93211; B93211; A93815; A94239; A01922; A01923
A;Accession: A93211
R;Seidman, J.G.; Max, E.E.; Leder, P.
Nature 280, 370-375, 1979
A;Title: A kappa-immunoglobulin gene is formed by site-specific recombination without f...
A;Cross-references: UNIPROT:P01639
A;Accession: B93211
A;Molecule type: DNA
A;Residues: 1-117 <VK41>
A;Cross-references: GB:V00804; GB:J00566; NID:g52127; PIDN:CAA24186.1; PID:g575660
R;Burstein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
A;Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursor
A;Reference number: A93815; MUID:77148916; PMID:403522
A;Accession: A93815
A;Molecule type: protein
A;Residues: 1-33 <BUR>
A;Note: Met-3 is apparently used as an alternative initiator in 25% of the chains
R;Gray, W.R.; Dreyer, W.J.; Hood, L.
Science 155, 465-467, 1967
A;Title: Mechanism of antibody synthesis: size differences between mouse kappa chains.
A;Reference number: A94239; MUID:67056897; PMID:4162931
A;Accession: A94239
A;Molecule type: protein
A;Residues: 23-49,'B',51-53,'LSB',57-58,'ZZ',61-62,'B2',65-76,'B',78-108,110-130 <GRA>
A;Experimental source: Bence Jones protein MOPC 41
C;Genetics:
A;Introns: 19/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka...
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: alternative initiators; heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status experimental <SIG1>
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F;23-22/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>
F;38-112/Domain: immunoglobulin homology <IMM>
F;45-110/Disulfide bonds: #status predicted

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Best Local Similarity 92.2%; Pred. No. 1.5e-42;
Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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Qy      1 MGAPAQIIGFLLLFLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60
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Db      3 MRAPAQIFGFLLLLFLFPQSTRCDIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQEP 62

Qy     61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
            |||||||||:|||| || |||||||||||||||||||||||||:|||||||||||||:||||
Db     63 DGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGG 122

Qy    121 GTKLEIKR 128
            ||||||||
Db    123 GTKLEIKR 130
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RESULT 2
PL0260
Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0260
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Molecule type: mRNA
A;Residues: 1-106 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-106/Region: framework 4

Query Match   67.7%; Score 501; DB 2; Length 106;
Best Local Similarity 93.4%; Pred. No. 8.9e-35;
Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Db      1 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQEPDGTIKRLIYATSSLDSGVPK 60

Qy     81 RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEI 126
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Db     61 RFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGGGTKLEI 106
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RESULT 3
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C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0259
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Molecule type: mRNA
A;Residues: 1-106 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-106/Region: framework 4

Query Match   67.0%; Score 496; DB 2; Length 234;
Best Local Similarity 68.5%; Pred. No. 5.1e-34;
Matches 98; Conservative 15; Mismatches 30; Indels 0; Gaps 0;

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Db      1 MRTPAQFIGILLLWFPGTKCDIQMTQSPSSMYASLGERVVTCKASQDINSYLSWIQKP 60

Qy     61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
            |||||||||:|||: |  |||||||||||||||||||||||||:|||||||||||||:||||
Db     61 GKSPKTLIYRGNRLAVGVPSRFSGSGSGQDYSLTISSLEYEDVGVYVYCLRYDEFPTFGS 120

Qy    121 GTKLEIKRADAAPTVSIFPPSSK 143
            ||||||| : : :::::||||::
Db    121 GTKLEIKRADAAPTVSIFPPSSE 143
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RESULT 4
S14237
Ig kappa chain precursor (15C5) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S14237
R;Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Eur. J. Biochem. 192, 767-775, 1990
A;Title: Construction and characterization of a recombinant murine monoclonal antibody d
A;Reference number: S14236; MUID:91006173; PMID:2209622
A;Molecule type: mRNA
A;Residues: 1-234 <VAN>
A;Cross-references: EMBL:X56394; NID:g951622; PIDN:CAA39805.1; PID:g951623
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match   67.2%; Score 497; DB 2; Length 106;
Best Local Similarity 92.5%; Pred. No. 1.9e-34;
Matches 98; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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Db      1 DIQMTQSPSSLSASLGERVSLTCRASQDIGINLHWLQEPDGTIKRLIYATSSLGSGVPK 60

Qy     81 RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEI 126
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RESULT 5
D32513
Ig kappa chain precursor V region (BXW16) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: D32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and
A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Molecule type: DNA
A;Residues: 1-129 <KOF>
A;Cross-references: GB:M20832; NID:g1965941; PIDN:AAA38845.1; PID:g1965942
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match   64.6%; Score 478; DB 2; Length 129;
Best Local Similarity 76.8%; Pred. No. 8.7e-33;
Matches 96; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

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            ::||| |:|  :::||  :  |:|| |||:||||||||||||||||||||||||||||||||
Db      3 APAQIIGFLLLFLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDG 62

Qy     61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
            ||||||||||||| || |||||||||||||||||||||||||||||||||||||||||||
Db     61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120

Qy    121 GTKLEIKRADAAPTVSIFPPSSE 143
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Db    121 GTKLEIKRADAAPTVSIFPPSSE 143
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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: December 6, 2004, 13:34:19 ; Search time 185.386 Seconds
(without alignments)
278.934 Million cell updates/sec

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Perfect score: 740
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	740	100.0	145	9	US-09-861-294-2	Sequence 2, Appli
2	740	100.0	145	14	US-10-367-506-2	Sequence 2, Appli
3	626	84.6	144	16	US-10-642-120-4	Sequence 4, Appli
4	626	84.6	144	16	US-10-642-060-4	Sequence 4, Appl
5	626	84.6	144	16	US-10-642-122-4	Sequence 4, Appl
6	626	84.6	144	16	US-10-642-124-4	Sequence 4, Appl
7	626	84.6	144	16	US-10-621-269-4	Sequence 4, Appl
8	626	84.6	144	16	US-10-620-850-4	Sequence 4, Appl
9	626	84.6	144	17	US-10-642-118-4	Sequence 4, Appl
10	626	84.6	144	17	US-10-642-117-4	Sequence 4, Appl
11	626	84.6	144	17	US-10-642-119-4	Sequence 4, Appl
12	626	84.6	144	17	US-10-642-099-4	Sequence 4, Appl
13	601	81.2	130	8	US-08-779-784-35	Sequence 35, Appl

14	601	81.2	130	14	US-10-010-729-71	Sequence 71, Appl
15	541	73.1	130	14	US-10-268-883-11	Sequence 11, Appl
16	518	70.0	129	8	US-08-973-518-2	Sequence 2, Appli
17	518	70.0	129	9	US-09-007-093-2	Sequence 2, Appli
18	510	70.0	129	14	US-10-428-754-2	Sequence 2, Appl
19	510	68.9	108	14	US-10-010-729-45	Sequence 45, Appl
20	507	68.5	243	9	US-09-887-853-6	Sequence 6, Appli
21	506	68.4	108	9	US-09-924-099-1	Sequence 1, Appli
22	505	68.2	252	15	US-10-239-656-55	Sequence 55, Appl
23	505	68.2	499	15	US-10-239-656-73	Sequence 73, Appl
24	505	68.2	108	16	US-10-803-2276B-4	Sequence 4, Appli
25	503	68.0	108	16	US-10-803-653-267	Sequence 267, App
26	503	68.0	108	16	US-10-038-591-48	Sequence 48, Appl
27	502	67.8	236	14	US-10-775-444A-48	Sequence 48, Appl
28	502	67.8	237	17	US-10-775-444A-48	Sequence 48, Appl
29	502	67.8	237	9	US-09-924-099-9	Sequence 9, Appli
30	502	67.8	243	9	US-09-924-099-10	Sequence 10, Appl
31	502	67.8	257	9	US-09-924-099-67	Sequence 67, Appl
32	501	67.7	234	15	US-10-239-656-97	Sequence 97, Appl
33	496	67.0	109	9	US-09-943-906-74	Sequence 74, Appl
34	496	67.0	109	14	US-10-435-602-74	Sequence 74, Appl
35	494	66.8	236	15	US-10-038-591-52	Sequence 52, Appl
36	494	66.8	236	17	US-10-775-444A-52	Sequence 52, Appl
37	493	66.6	234	16	US-10-684-109-115	Sequence 115, App
38	488	65.9	234	16	US-10-684-109-91	Sequence 91, Appl
39	488	65.9	234	16	US-10-684-109-109	Sequence 109, Appl
40	486	65.7	234	16	US-10-684-109-103	Sequence 103, App
41	479	64.7	148	16	US-10-222-026A-25	Sequence 25, Appl
42	479	64.7	287	16	US-10-222-026A-37	Sequence 37, Appl
43	475	64.2	236	15	US-10-038-591-51	Sequence 51, Appl
44	475	64.2	236	17	US-10-775-444A-51	Sequence 51, Appl
45	474	64.1	234	14	US-10-292-088-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-861-294-2
; Sequence 2, Application US/09861294
; Patent No. US2002009819OA1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 3041420000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 2
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-09-861-294-2

Query Match 100.0%; Score 740; DB 9; Length 145;
Best Local Similarity 100.0%; Pred. No. 5.8e-55;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60
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Qy 61 DGTIKRLIYATSSLSGSVPKRFSGSRSGSDYSLTISSLESBDFVAYYCLQYASSPYTFGG 120

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RESULT 2
US-10-367-506-2
; Sequence 2, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 3041420000620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-367-506-2

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Best Local Similarity 100.0%; Pred. No. 5.8e-55;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60
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RESULT 3
US-10-642-120-4
; Sequence 4, Application US/10642120
; Publication No. US20040131610A1
; GENERAL INFORMATION:
; APPLICANT: Thorpe, Philip E.
; APPLICANT: Soares, M. Melina
; APPLICANT: Ran, Sophia
; TITLE OF INVENTION: Methods for Treating Viral Infections Using Antibodies to
; TITLE OF INVENTION: Aminophospholipids
; FILE REFERENCE: 4001.002900
; CURRENT APPLICATION NUMBER: US/10/642,120
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/621,269
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,263
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-120-4

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Matches 125; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

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RESULT 4
US-10-642-060-4
; Sequence 4, Application US/10642060
; Publication No. US20040131621A1
; GENERAL INFORMATION:
; APPLICANT: Thorpe, Philip E.
; APPLICANT: Soares, M. Melina
; APPLICANT: Ran, Sophia
; TITLE OF INVENTION: Combinations and Kits for Treating Viral Infections Using Antibod
; FILE REFERENCE: 4001.002982
; CURRENT APPLICATION NUMBER: US/10/642,060
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/621,269
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,263
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-060-4

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Matches 125; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

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Qy       121 GTKLEIKRADAAPTVSIF 138
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Db       123 GTKLELKRADAAPTVFIF 140
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RESULT 5
US-10-642-122-4
; Sequence 4, Application US/10642122
; Publication No. US20040131622A1
; GENERAL INFORMATION:
; APPLICANT: Thorpe, Philip E.
; APPLICANT: Soares, M. Melina
; APPLICANT: Ran, Sophia

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

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Maximum Match 100%
Listing first 45 summaries

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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

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2	.435	100.0	435	15	US-10-367-506-1	Sequence 1, Appli
3	384.6	88.4	407	9	US-09-924-099-27	Sequence 27, Appl
4	372.4	85.6	435	17	US-10-642-120-3	Sequence 3, Appl
5	372.4	85.6	435	17	US-10-642-060-3	Sequence 3, Appli
6	372.4	85.6	435	17	US-10-642-122-3	Sequence 3, Appli
7	372.4	85.6	435	17	US-10-642-124-3	Sequence 3, Appli
8	372.4	85.6	435	17	US-10-621-269-3	Sequence 3, Appl
9	372.4	85.6	435	17	US-10-620-850-3	Sequence 3, Appl
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12	372.4	85.6	435	18	US-10-642-119-3	Sequence 3, Appli
13	372.4	85.6	435	18	US-10-642-099-3	Sequence 3, Appli
14	372	85.5	402	8	US-08-779-784-5	Sequence 5, Appli
15	372	85.5	402	8	US-10-010-729-5	Sequence 5, Appli
16	329.6	75.8	390	15	US-10-268-883-10	Sequence 10, Appl
17	323.4	74.3	387	8	US-08-973-518-1	Sequence 1, Appli
18	323.4	74.3	387	8	US-09-007-093-1	Sequence 1, Appli
19	323.2	74.3	387	15	US-10-428-754-1	Sequence 1, Appli
20	323.2	74.3	351	8	US-08-779-788-17	Sequence 17, Appl
21	322.6	74.2	351	8	US-08-779-784-16	Sequence 16, Appl
22	311.2	71.5	324	15	US-10-010-729-46	Sequence 46, Appl
23	309.4	71.1	739	9	US-09-887-853-5	Sequence 5, Appl
24	308.4	70.9	729	9	US-09-924-099-20	Sequence 20, Appl
25	307.4	70.7	711	9	US-09-924-099-19	Sequence 19, Appl
26	306.4	70.4	324	9	US-09-924-099-11	Sequence 11, Appl
27	301.4	69.3	756	16	US-10-239-656-54	Sequence 54, Appl
28	301.4	69.3	771	16	US-10-239-656-66	Sequence 66, Appl
29	301.4	69.3	324	17	US-10-222-026A-26	Sequence 26, Appl
30	292	67.1	1497	16	US-10-307-276B-2	Sequence 2, Appl
31	284.4	65.4	456	17	US-10-222-026A-38	Sequence 38, Appli
32	282.4	64.9	867	16	US-10-239-656-72	Sequence 72, Appl
33	268.4	61.7	463	16	US-10-395-894-24	Sequence 24, Appl
34	268.4	61.7	463	16	US-10-695-667-24	Sequence 24, Appl
35	268.4	61.7	702	17	US-10-684-109-89	Sequence 89, Appl
36	268.4	61.7	702	17	US-10-684-109-90	Sequence 90, Appl
37	268.4	61.7	702	17	US-10-684-109-95	Sequence 95, Appli
38	268.4	61.7	702	17	US-10-684-109-96	Sequence 96, Appli
39	268.4	61.7	702	17	US-10-684-109-107	Sequence 107, Appl
40	268.4	61.7	702	17	US-10-684-109-108	Sequence 108, Appl
41	268.4	61.7	702	17	US-10-684-109-113	Sequence 113, Appl
42	268.4	61.7	702	17	US-10-684-109-114	Sequence 114, App
43	268.4	61.7	16	16	US-10-395-894-10	Sequence 10, Appl
44	268.4	61.7	6082	16	US-10-695-667-10	Sequence 10, Appl
45	267.6	61.5	447	9	US-09-797-481-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-861-294-1

; Sequence 1, Application US/09861294
; Patent No. US2002009819oA1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 30414200006Z0
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 1
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(435)
; NAME/KEY: sig_peptide
; LOCATION: (1)...(60)
; NAME/KEY: mat_peptide
; LOCATION: (61)...(435)
US-09-861-294-1

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Best Local Similarity　　100.0%;
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RESULT 2
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; Sequence 1, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
;
SEQ ID NO 1
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(435)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(60)
; FEATURE:
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; LOCATION: (61)...(435)
US-10-367-506-1

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Best Local Similarity   100.0%;
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; Sequence 27, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: OKURA, Yoshihiro
; APPLICANT: NISHIDA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
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; LENGTH: 407
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(407)
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; NAME/KEY: sig_peptide
; LOCATION: (1)...(60)
US-09-924-099-27

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Best Local Similarity   96.6%; Pred. No. 3.7e-117;
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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: December 6, 2004, 13:29:00 ; Search time 15.5705 Seconds
(without alignments)
617.586 Million cell updates/sec

Title: US-08-836-455-2
Perfect Score: 740
Sequence: 1 MGAPAQILGFLLLLFPGTRC..........IKRADAAPTVSIFPPSSKLG 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	518	70.0	129	3	US-08-973-518-2	Sequence 2, Appli
4	507	68.5	243	1	US-08-133-804-6	Sequence 6, Appl
5	507	68.5	243	2	US-08-461-838-6	Sequence 6, Appli
6	507	68.5	243	2	US-08-461-386-6	Sequence 6, Appli
7	507	68.5	243	2	US-08-356-786-4	Sequence 4, Appli
8	503	68.0	534	2	US-08-356-786-10	Sequence 10, Appl
9	496	67.0	109	2	US-08-713-939A-74	Sequence 74, Appl
10	496	67.0	109	3	US-09-036-579-74	Sequence 74, Appl
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12	496	67.0	109	4	US-09-943-906-74	Sequence 74, Appl
13	492	66.5	107	2	US-08-483-749A-26	Sequence 26, Appl
14	483	65.3	138	2	US-08-480-434-63	Sequence 63, Appl
15	483	65.3	138	2	US-08-053-451B-63	Sequence 63, Appl
16	479	64.7	148	2	US-09-318-786-25	Sequence 25, Appl
17	479	64.7	236	1	US-08-157-101A-5	Sequence 5, Appl
18	479	64.7	287	4	US-09-318-786-37	Sequence 37, Appl
19	471	63.6	112	2	US-09-627-218B-1	Sequence 1, Appl
20	471	63.6	142	2	US-08-579-940-2	Sequence 2, Appl
21	471	63.6	142	3	US-08-838-692-4	Sequence 4, Appl
22	468	63.2	142	2	US-08-888-366-14	Sequence 14, Appli
23	468	63.2	107	2	US-08-888-366-20	Sequence 20, Appl
24	463	62.6	107	1	US-08-888-366-26	Sequence 26, Appl
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26	461	62.3	131	5	PCT-US95-05262-2	Sequence 2, Appli
27	455	61.5	109	1	US-07-942-245-1	Sequence 1, Appli
28	455	61.5	127	4	US-09-647-468-183	Sequence 183, App
29	454	61.4	127	4	US-09-647-468-182	Sequence 182, App
30	451	60.9	127	4	US-09-647-468-180	Sequence 180, App
31	447	60.4	127	4	US-09-647-468-179	Sequence 179, App
32	447	60.4	129	4	US-09-647-468-161	Sequence 161, Appl
33	445	60.3	234	4	US-09-740-002-24	Sequence 24, Appl
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35	444	60.0	127	2	US-08-458-516-5	Sequence 5, Appli
36	442	59.7	127	1	US-08-713-939A-73	Sequence 73, Appl
37	442	59.7	109	3	US-09-036-579-73	Sequence 73, Appl
38	442	59.7	109	4	US-09-550-374-73	Sequence 73, Appl
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41	441	59.6	127	2	US-08-137-117D-29	Sequence 29, Appl
42	441	59.6	127	1	US-08-437-717-29	Sequence 29, Appl
43	441	59.6	235	3	US-08-812-586-16	Sequence 16, Appl
44	441	59.6	235	4	US-09-535-832A-17	Sequence 17, Appl
45	439	59.3	127	4	US-09-647-468-162	Sequence 162, App

ALIGNMENTS

RESULT 1
US-09-096-244-2
Sequence 2, Application US/09096244
Patent No. 6274143

; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
; TITLE OF INVENTION: HMFG-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 11D10
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION NUMBER: US/09/096,244
; APPLICATION NUMBER: US/09/096,244
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Polizzi, Catherine M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 30414-20006.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-096-244-2

Query Match   100.0%; Score 740; DB 3; Length 145;
Best Local Similarity   100.0%; Pred. No. 5.6e-63;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   61 DGTIKRLIYATSSLGSGVPKRFSGSRSGGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
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Qy   121 GTKLEIKRADAAPTVSIFPPSSKLG 145
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Db   121 GTKLEIKRADAAPTVSIFPPSSKIG 145

RESULT 2
US-08-943-136-2
Sequence 2, Application US/08943136
; Patent No. 6291208
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,136
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,576
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-733
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-943-136-2

Query Match   70.0%; Score 518; DB 3; Length 129;
Best Local Similarity   80.3%; Pred. No. 6.2e-42;
Matches 102; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

Qy   1 MGAPAQIIGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP   60
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Db   3 MRVPAHVFGFLLLWFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQEISGYLTWLQQKP   62

Qy   61 DGTIKRLIYATSSLGSGVPKRFSGSRSGGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
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Db   63 DGTIKRLVYAASTLDSGVPKRFSGSRSGSDTSLTISSLESEDFADYYCLQYTNYPLTFGA   122

Qy   121 GTKLEIK 127
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Db   121 GTKLELK 129

RESULT 3
US-08-973-518-2
Sequence 2, Application US/08973518
; Patent No. 6328962
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,518
; FILING DATE: 07-APR-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-973-518-2

Query Match   70.0%; Score 518; DB 3; Length 129;
Best Local Similarity   80.3%; Pred. No. 6.2e-42;
Matches 102; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

Qy   1 MGAPAQIIGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP   60
            || : ||||||||||||||||||||||||||||||||||||||||||||||| |||:|
Db   3 MRVPAHVFGFLLLWFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQEISGYLTWLQQKP   62

Qy   61 DGTIKRLIYATSSLGSGVPKRFSGSRSGGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
            ||||||||:|| |:| ||||||||||||||||||||||||||||||||||||:||| :|
Db   63 DGTIKRLVYAASTLDSGVPKRFSGSRSGSDTSLTISSLESEDFADYYCLQYTNYPLTFGA   122

Qy   121 GTKLEIK 127
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Db   121 GTKLELK 129

RESULT 4
US-08-133-804-6
Sequence 6, Application US/08133804
; Patent No. 5534254
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging

OM protein - protein search, using sw model

Run on: December 6, 2004, 13:29:00 ; Search time 52.0638 seconds
                                          (without alignments)
                                          999.078 Million cell updates/sec

                GenCore version 5.1.6
                Copyright (c) 1993 - 2004 Compugen Ltd.

Title: US-08-836-455-2
Perfect score: 740
Sequence: 1 MGAPAQILGFLLLLFPGTRC........IKRADAAPTVSIFPPSSKLG 145

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5
Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_23Sep04:*
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               2: geneseqp1990s:*
               3: geneseqp2000s:*
               4: geneseqp2001s:*
               5: geneseqp2002s:*
               6: geneseqp2003a:*
               7: geneseqp2003ba:*
               8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match Length	DB	ID	Description
1	740	100.0	145	2	AAW27119	Aaw27119 Murine mo
2	740	100.0	145	6	AAO16292	Aao16292 Mouse 11D
3	727	98.2	145	2	AAW87593	Aaw87593 Antibody
4	662	89.5	146	1	AAP30251	Aap30251 Sequence
5	645	87.2	153	8	ADJ57089	Adj57089 3G4-2BVL-
6	633	85.5	135	3	AAY44599	Aay44599 Mouse lig
7	626	84.6	144	8	AAJ57086	Aaj57086 Mouse 3G4 antib
8	601	81.2	130	8	ADI26651	Adi26651 Human ant
9	541	73.1	130	6	AAO23070	Aao23070 Human ant
10	527	71.2	129	2	AAW22537	Aaw22537 Murine an
11	527	71.2	129	5	AAE20200	Aae20200 Murine 44
12	527	71.2	129	8	ADJ31873	Adj31873 Murine 44
13	518	70.0	129	5	AAE20204	Aae20204 Murine 44
14	510	68.9	108	2	ADI26702	Adi26702 Mouse ant
15	508	68.6	246	2	AAR39569	Aar39569 Sequence
16	507	68.5	243	2	AAW02280	Aaw02280 520C9 ant
17	507	68.5	243	2	AAW53170	Aaw53170 520C9 ant
18	507	68.5	243	2	AAW80424	Aaw80424 520C9 sFv
19	507	68.5	243	7	ABW00716	Abw00716 520C9 sFv
20	506	68.4	108	5	AAY44587	Aay44587 Mouse
21	505	68.2	252	5	AAU72863	Aau72863 P4-14 sin
22	505	68.2	499	5	AAU72872	Aau72872 3B10xP4-1
23	504	68.1	107	2	AAW27121	Aaw27121 Murine an
24	503	68.0	108	2	AAR21310	Aar21310 Light cha
25	503	68.0	108	8	AD060443	Ad060443 Mouse ant
26	503	68.0	144	2	AAR15322	Aar15322 IL-2 chim
27	503	68.0	146	4	AAB99115	Aab99115 Human pro
28	503	68.0	146	4	ABG77160	Abg77160 Germline
29	502	67.8	237	3	AAY44595	Aay44595 EscFvH125
30	502	67.8	243	3	AAY44596	Aay44596 EscFvH125
31	502	67.8	257	7	AAU72869	Aau72869 P5-11 sin
32	501	67.7	237	7	ADE57549	Ade57549 Human Pro
33	501	67.7	237	7	ADD47098	Add47098 Human Pro
34	501	67.7	237	2	ADD48668	Add48668 Human Pro
35	497	67.2	144	2	AAR15321	Aar15321 IL-2 chim
36	496	67.0	109	2	AAW18271	Aaw18271 PrP 37 li
37	496	67.0	109	4	AAW85910	Aaw85910 PrP 37 li
38	496	67.0	109	2	AAG65862	Aag65862 Anti-PrP
39	496	67.0	109	4	ABP51796	Abp51796 Anti-prio
40	496	67.0	109	5	ABU58877	Abu58877 Anti-prio
41	495	66.9	534	2	AAR39571	Aar39571 Sequence
42	494	66.8	236	5	ABG77164	Abg77164 Germline
43	492	66.5	236	3	AAY90824	Aay90824 520C9 hyb
44	488	65.9	107	6	ABR55333	Abr55333 Amino aci
45	486	65.7	236	8	ADP07905	Adp07905 Human imm

ALIGNMENTS

RESULT 1
AAW27119
ID   AAW27119 standard; protein; 145 AA.
XX
AC   AAW27119;
XX
DT   25-MAR-2003   (revised)
DT   04-JAN-1998   (first entry)
XX
DE   Murine monoclonal anti-idiotype antibody 11D10 VL region.
XX
KW   Monoclonal antibody 11D10; anti-idiotype antibody; mucin;
KW   human milk fat globule; HMFG; tumour; breast cancer; vaccine.
OS   Mus musculus.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..20
FT   /label= Sig_peptide
FT   Protein   21..145
FT   /label= Mat_protein
FT   Region   21..43
FT   /label= FR1
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FT   /label= CDR1
FT   /note= "complementarity determining region 1"
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FT   /label= FR2
FT   /note= "framework region 2"
FT   Region   70..76
FT   /label= CDR2
FT   /note= "complementarity determining region 2"
FT   Region   77..108
FT   /label= FR3
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FT   Region   118..127
FT   /label= FR1
FT   /note= "framework region 4"
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PN   WO9722699-A2.
XX
PD   26-JUN-1997.
XX
PF   19-DEC-1996; 96WO-US020757.

XX
PR 20-DEC-1995; 95US-0057762;
PR 26-JAN-1996; 96US-00591965.
PR 13-DEC-1996; 96US-0076350.
XX
PA (KENT) UNIV KENTUCKY.
XX
PI Chatterjee M, Foon KA, Chatterjee SK;
XX
DR WPI; 1997-341690/31.
DR N-PSDB; AAT85149.
XX
PT Monoclonal anti-idiotype antibody 11D10 - elicits immune response against human milk fat globule disease associated tumours, especially breast cancer.
XX
PS Claim 9; Page 94; 130pp; English.
XX
CC This polypeptide sequence comprises the light chain variable region (VL) of monoclonal anti-idiotype antibody 11D10 produced by hybridoma cell line ATCC 12020. 11D10 was obtained by immunising naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype response. It elicits an immune response against a specific epitope of a high mol.wt. mucin of human milk fat globule (HMFG). It induces an immunological response to HMFG in mice, rabbits, monkeys and patients with advanced HMFG-associated tumours. Pharmaceutical compositions and vaccines comprising 11D10, 11D10 polypeptides and/or 11D10 polynucleotides (see also AAT85149-50) are claimed. Also claimed are diagnostic kits and methods of using 11D10, 11D10 polypeptides and/or 11D10 polynucleotides, including methods of treating HMFG-associated tumours. 11D10 is also used in a claimed method of palliating HMFG-associated tumours and in claimed kits to detect or quantify anti-HMFG antibody. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 145 AA;

Query Match   100.0%;   Score 740;   DB 2;   Length 145;
Best Local Similarity   100.0%;
Matches 145;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy    1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60

Qy   61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120

Qy  121 GTKLEIKRADAAPTVSIFPPSSKLG 145
        |||||||||||||||||||||||||
Db  121 GTKLEIKRADAAPTVSIFPPSSKLG 145
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RESULT 2
AA016292
ID AA016292 standard; protein; 145 AA.
XX
AC AA016292;
XX
DT 20-MAR-2003 (first entry)
XX
DE Mouse 11D10 antibody light chain variable region.
XX
KW Mouse; murine; vaccine; tumour; human milk fat globules; HMFG; carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour; CEA-associated tumour; anti-idiotype antibody.
OS Mus musculus.
XX
FH Key   Location/Qualifiers
FT Peptide   1..20
FT   /label= signal_peptide
FT Protein   21..145

FT   /note= "Mature murine 11D10 antibody light chain variable region"
XX
PN WO200292012-A2.
XX
PD 21-NOV-2002.
XX
PF 17-MAY-2002; 2002WO-US015840.
XX
PR 17-MAY-2001; 2001US-00861294.
XX
PA (KENT) UNIV KENTUCKY RES FOUND.
XX
PI Chatterjee M, Foon KA;
XX
DR WPI; 2003-129216/12.
DR N-PSDB; AAL51273.
XX
PS Claim 2; Fig 1; 98pp; English.
XX
PT Use of anti-idiotypic antibodies for human milk fat globules (HMFG)- or carcinoembryonic antigen (CEA)-associated tumor for delaying the development of, or treating a HMFG- or CEA-associated tumor (e.g. breast tumor) in humans.
XX
CC The invention comprises a method for delaying the development of, or treating a tumour that is associated with human milk fat globule (HMFG) or carcinoembryonic antigen (CEA). The method of the invention involves administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for delaying the development, of or treating HMFG/CEA-associated tumours. The present amino acid sequence represents the light chain variable region of the mouse 11D10 anti-idiotype antibody
XX
SQ Sequence 145 AA;

Query Match   100.0%;   Score 740;   DB 6;   Length 145;
Best Local Similarity   100.0%;
Matches 145;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy   61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120

Qy  121 GTKLEIKRADAAPTVSIFPPSSKLG 145
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Db  121 GTKLEIKRADAAPTVSIFPPSSKLG 145
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RESULT 3
AAW87593
ID AAW87593 standard; protein; 145 AA.
XX
AC AAW87593;
XX
DT 16-MAR-1999 (first entry)
XX
DE Antibody 11D10 light chain variable region.
XX
KW Murine; mouse; antibody; light chain; variable region; anti-idiotype; human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
OS Mus sp.
XX
FH Key   Location/Qualifiers
FT Peptide   1..20
FT   /note= "signal peptide"
FT Protein   21..999
FT   /note= "mature protein"

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 13:38:19 ; Search time 2233.74 Seconds
(without alignments)
7096.283 Million cell updates/sec

Title: US-08-836-455-1
Perfect score: 435
Sequence: 1 ATGGGGGGCCCCTGCTCAGAT...........CACCATCCAGTAAGCTTGGG 435
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 32828875 seqs, 1821865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	373.2	85.8	630	2	BF138788	BF138788 601780387
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3	334	76.8	714	4	BG963548	BG963548 602831226
4	320.2	73.6	374	5	BY083003	BY083003
5	287.8	66.2	827	4	BI152061	BI152061 602916512
6	287.6	66.1	874	4	BG518527	BG518527 602578261
7	286.0	65.9	891	2	BF579422	BF579422 602093833
8	285.2	65.6	626	2	BF582283	BF582283 602101109
9	285.2	65.6	725	2	BF580940	BF580940 602100636
10	282.8	65.0	1459	5	BQ918407	BQ918407
11	278.8	64.1	762	2	BF144806	BF144806 601791486
12	278		901	5	BQ943305	BQ943305 AGENCOURT
13	276.4	63.9	772	2	BF581992	BF581992 602099448
14	276.4	63.5	830	4	BI455041	BI455041 603173343
15	275.6	63.5	695	2	BE284224	BE284224 601099161
16	274.8	63.2	669	2	BF123422	BF123422 601760623
17	274.8	63.2	708	4	BI103114	BI103114 602889345
18	273.2	62.8	886	4	BG756818	BG756818 602710291
19	269.2	61.9	658	6	CF108834	CF108834 Shultzomi
20	268.0	61.8	685	4	BG518543	BG518543 602578277
21	268.0	61.8	617	6	CD699887	CD699887
22	266.8	61.3	697	6	CD699896	CD699896
23	266.8	61.3	698	6	CD691710	CD691710 EST8233 h
24	266.8	61.3	952	7	CO579354	CO579354 ILLUMIGEN
25	266.8	61.3	969	5	BU899279	BU899279 AGENCOURT
26	265.2	61.0	464	5	BX480430	BX480430 DKFZp686E
27	265.2	61.0	547	5	CD704894	CD704894 EST21421
28	265.2	61.0	764	6	CB956251	CB956251 AGENCOURT
29	265.2	61.0	1019	4	BM914405	BM914405 AGENCOURT
30	264.4	60.8	354	5	BY085718	BY085718 BY085718
31	263.6	60.6	545	5	CD697196	CD697196 EST13719
32	263.6	60.6	550	5	CD709576	CD709576 EST12160
33	263.6	60.6	586	6	CD695617	CD695617 EST12140
34	263.6	60.6	658	5	CD701345	CD701345 AGENCOURT
35	263.6	60.6	723	5	CB956143	CB956143 AGENCOURT
36	263.6	60.6	992	2	BF976253	BF976253 602245130
37	263.6	60.4	851	4	BI101548	BI101548 602887347
38	262.8	60.4	1038	2	BF757218	BF757218 602710591
39	262.2	60.3	966	2	BF578083	BF578083 602094759
40	262	60.2	569	6	CD706691	CD706691 EST23218
41	262	60.2	616	6	CD684315	CD684315 EST8335 hu
42	262	60.2	666	6	CD684691	CD684691 EST12211 h
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RESULT 1

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BF138788
LOCUS       BF138788                 630 bp    mRNA    linear   EST 24-OCT-2000
DEFINITION  601780387F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4008404 5',
            mRNA sequence.
ACCESSION   BF138788
VERSION     BF138788.1  GI:10977828
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 630)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by:Incyte Genomics, Inc.
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9242 row: n  column: 21
            High quality sequence stop: 628.
FEATURES             Location/Qualifiers
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                     Site 2: SalI; transgenic model WNT-1, expression driven by
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                     dT. Library constructed by Life Technologies.
                     Investigator providing samples: Gilbert Smith, NIH"
ORIGIN
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ALIGNMENTS

Query Match 85.8%; Score 373.2; DB 2; Length 630;
Best Local Similarity 92.3%;
Matches 393; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

RESULT 2

Qy   5 GGGGCCCCTGCTGTCAGATTCTTGGGTTCTTGTTGTTGCTTCTTGTTTGTTTCCAGGTACCAGAGATGTGACA 64
           ||||||||| || || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGGCTCCTGCCGCAGGTTTTGGCTTCTTGTTGCTTCTTGTTTGTTTCCAGGTGCCAGAGATGTGACA 60

Qy   65 TCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTTCTGGGGACAAAGAGTCAGTCTCTCA 124
           ||||||||||||||| |||| |||||||||||||||| ||||||||||||||||| ||||||||||
Db   61 .TCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTTCTGGGGACAAAGAGTCACAGATGTCA 120

Qy   125 CTTGTCGGGGCAAGTCAGGGACAATTGGTATTAACTTACATTGGCTTCAGCAGGAACCAGATG 184
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CTTGCCGGGGCAAGTCAGGGACAATTGGTGTGTTAAACTGGTTTCAGCAGAAACCAGATG 180

Qy   185 GAACTATTAAACGCCTGATCTACGGCCACATCCAGTTTAGGTTCTGTGGTCCCCAAAAGGT 244
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GAACTATTAAACGCCTGATCTACGGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGGT 240

Qy   245 TCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCCACCAATCAGCGACGCCTTGAGTCTGAAG 304
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Qy   305 ATTTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTTCCGGTACACGTTTCGGAGGGGGGA 364
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DEFINITION 602829953F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4984788 5',
            mRNA sequence.
ACCESSION   BG962572
VERSION   BG962572.1 GI:14350209
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 926)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10991 row: i column: 13
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            /lab host="DH10B (T1 phage-resistant)"
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            /organism="Mus musculus"
            /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
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ORIGIN   Technologies. Note: this is a NCI_CGAP Library."

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Best Local Similarity 90.2%; Pred. No. 4.6e-104;
Matches 388; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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Qy   121 CTCACTTGTCGGGGCAAGTCAGGGACAATTGGTATTAACTTACATTGGCTTCAGCAGGAACCA 180
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RESULT 3
LOCUS   BG963548   714 bp   mRNA   linear   EST 12-JUN-2001
DEFINITION 602831226F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4985791 5',
            mRNA sequence.
ACCESSION   BG963548
VERSION   BG963548.1 GI:14351185
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 714)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10994 row: c column: 08
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                     /strain="FVB/N"
                     /db_xref="taxon:10090"

GenCore version 5.1.6
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Perfect score: 435
Sequence:　　1 ATGGGGGGCCCCTGCTCAGAT............CACCATCCAGTAAGCTTGGG 435

Scoring table: IDENTITY_NUC
Scoring table: Gapop 10.0 , Gapext 1.0

Searched:　　824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters:　　1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	323.4	74.3	387	3	US-08-943-136-1	Sequence 1, Appli
3	323.4	74.3	387	2	PCT-US95-05262-1	Sequence 1, Appli
4	309.4	71.1	732	3	US-08-973-518-1	Sequence 1, Appli
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6	309.4	71.1	739	1	US-08-133-804-5	Sequence 5, Appli
7	309.4	71.1	739	1	US-08-461-386-5	Sequence 5, Appli
8	305.2	70.2	1605	2	US-08-356-786-9	Sequence 9, Appli
9	300.2	69.0	321	3	US-08-483-749A-25	Sequence 25, Appl
10	292.2	67.2	321	3	US-08-888-366-13	Sequence 13, Appl
11	292.2	67.2	321	2	US-08-888-366-19	Sequence 19, Appl
12	291.2	66.9	321	2	US-08-888-366-25	Sequence 25, Appl
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14	282.4	64.9	867	4	US-08-456-786-38	Sequence 38, Appl
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16	267.6	61.5	447	1	US-08-838-692-3	Sequence 3, Appli
17	266.6	61.3	321	3	US-08-483-749A-27	Sequence 27, Appl
18	265.2	61.0	449	1	US-08-480-434-61	Sequence 61, Appl
19	265.2	61.0	449	1	US-09-472-087-62	Sequence 62, Appl
20	263.6	60.6	714	4	US-08-053-451B-61	Sequence 61, Appl
21	263.2	60.5	276	2	US-08-273-146-52	Sequence 52, Appl
22	262	60.2	439	3	US-08-273-146-52	Sequence 52, Appl
23	262	60.2	439	3	US-05-042-353-360	Sequence 360, App
24	261.6	60.2	276	2	US-08-758-417A-208	Sequence 208, App
25	260.4	59.9	1066	2	US-08-157-101A-4	Sequence 44, Appli
26	258.8	59.5	751	5	PCT-US94-07659-3	Sequence 4, Appli
27	258.8	59.5	3819	3	US-09-042-353-393	Sequence 393, App
28	258.8	59.5	3819	3	US-08-758-417A-243	Sequence 243, App
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30	258.6	59.4	393	5	US-08-236-520-1	Sequence 1, Appli
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32	252	57.9	381	1	US-08-137-117D-28	Sequence 28, Appl
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ALIGNMENTS

RESULT 1
US-09-096-244-1
Sequence 1, Application US/09096244
Patent No. 6274143

GENERAL INFORMATION:
　APPLICANT: Chatterjee, Malaya
　APPLICANT: Foon, Kenneth A.
　TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
　TITLE OF INVENTION: HMFG-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 11D10
　NUMBER OF SEQUENCES: 4
　CORRESPONDENCE ADDRESS:
　ADDRESSEE: MORRISON & FOERSTER
　STREET: 755 PAGE MILL ROAD
　CITY: PALO ALTO
　STATE: CA
　COUNTRY: USA
　ZIP: 94304-1018
　COMPUTER READABLE FORM:
　MEDIUM TYPE: Floppy disk
　COMPUTER: IBM PC compatible
　OPERATING SYSTEM: PC-DOS/MS-DOS
　SOFTWARE: Patentin Release #1.0, Version #1.30
　CURRENT APPLICATION DATA:
　APPLICATION NUMBER: US/09/096,244
　FILING DATE:
　CLASSIFICATION:
　ATTORNEY/AGENT INFORMATION:
　NAME: Polizzi, Catherine M.
　REGISTRATION NUMBER: 40,130
　REFERENCE/DOCKET NUMBER: 30414-20006.00
　TELECOMMUNICATION INFORMATION:
　TELEPHONE: (650) 813-5600
　TELEFAX: (650) 494-0792
　TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
　SEQUENCE CHARACTERISTICS:
　LENGTH: 435 base pairs
　TYPE: nucleic acid
　STRANDEDNESS: single
　TOPOLOGY: linear
　MOLECULE TYPE: DNA (genomic)
　FEATURE:
　NAME/KEY: CDS
　LOCATION: 1..435
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　NAME/KEY: mat_peptide
　LOCATION: 61
US-09-096-244-1

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Best Local Similarity 100.0%; Pred. No. 7.8e-132;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-08-943-136-1
Sequence 1, Application US/08943136
Patent No. 629208

; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,136
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 536
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 536
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,576
; FILING DATE:
; CLASSIFICATION:
; COMPUTER READABLE FORM:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-733

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-943-136-1

Query Match 74.3%; Score 323.4; DB 3; Length 387;
Best Local Similarity 90.6%; Pred. No. 1.5e-95;
Matches 345; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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RESULT 3
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Sequence 1, Application US/08973518
Patent No. 6328962

; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,518
; FILING DATE: 07-APR-1998
; CLASSIFICATION:

OM nucleic - nucleic search, using sw model

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Run on: December 6, 2004, 13:36:24 ; Search time 333.047 Seconds
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6856.387 Million cell updates/sec

Title: US-08-836-455-1
Perfect score: 435
Sequence: 1 ATGGGGGGCCCCTGCTCAGAT...........CACCATCCAGTAAGCTTGGG 435
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4134886 seqs, 262471O521 residues
Total number of hits satisfying chosen parameters: 8269772
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	382.2	87.9	842	12	ADK67935	Adk67935 Mouse cDN
7	372.4	85.6	435	12	ADJ57087	Adj57087 3G4 antib
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20	309.4	71.1	739	10	AAD61485	Aad61485 520C9 8Fv
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24	306.4	70.4	324	3	AAZ49534	Aaz49534 Mouse ant
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26	301.4	69.4	756	6	AAS97136	Aas97136 Sequence
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29	300.2	69.0	321	3	AAA38908	Aaa38908 520C9 hyb
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31	292	67.1	321	3	AAQ97507	Aaq97507 Light cha
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34	284.4	65.4	432	2	AAQ15114	Aaq15114 IL-2 chim
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38	273	62.8	297	12	ADM78076	Adm78076 Human SJA
39	270	62.1	981	12	ADP07904	Adp07904 Human imm
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41	269.2	61.7	438	4	AAH41157	Aah41157 Human cod
42	268.4	61.7	463	4	AAD56221	Aad56221 Human AB-
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ALIGNMENTS

RESULT 1
AAT85149
ID   AAT85149 standard; cDNA; 435 BP.
XX
AC   AAT85149;
XX
DT   25-MAR-2003 (revised)
DT   04-JAN-1998 (first entry)
XX
DE   Murine monoclonal anti-idiotype antibody 11D10 VL cDNA.
XX
KW   Monoclonal antibody 11D10; anti-idiotype antibody; mucin;
KW   human milk fat globule; HMFG; tumour; breast cancer; vaccine; ss.
XX
OS   Mus musculus.
XX
FH   Key   Location/Qualifiers
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PN   WO9722699-A2.
XX
PD   26-JUN-1997.
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PF   19-DEC-1996; 96WO-US020757.
XX
PR   20-DEC-1995; 95US-00575762.
PR   26-JAN-1996; 96US-00591965.
PR   13-DEC-1996; 96US-00765350.
XX
PA   (KENT) UNIV KENTUCKY.
XX
PI   Chatterjee M, Foon KA, Chatterjee SK;
XX
DR   WPI; 1997-341690/31.
DR   P-PSDB; AAW27119.
XX
PT   Monoclonal anti-idiotype antibody 11D10 - elicits immune response against
PT   human milk fat globule disease associated tumours, especially breast
PT   cancer.
XX
PS   Claim 11; Page 94; 130pp; English.

XX
CC This cDNA sequence encodes the light chain variable region VL (AAW85149)
CC of monoclonal anti-idiotype antibody 11D10 produced by hybridoma cell
CC line ATCC 12020. 11D10 was obtained by immunising naive mice with MC-10
CC anti-HMFG antibody to obtain an anti-idiotype response. It elicits an
CC immune response against a specific epitope of a high mol.wt. mucin of
CC human milk fat globule (HMFG). It induces an immunological response to
CC HMFG in mice, rabbits, monkeys and patients with advanced HMFG-associated
CC tumours. Pharmaceutical compositions and vaccines comprising 11D10,
CC polypeptides and/or 11D10 polynucleotides are claimed. Also claimed are
CC diagnostic kits and methods of using 11D10, 11D10 polypeptides and/or
CC 11D10 polynucleotides, including methods of treating HMFG- associated
CC tumours. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 U; 0 Other;

Query Match   100.0%; Score 435; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 5.6e-127;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    61 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGACAGAGTCAGT 120
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Qy   121 CTCACTTGTCGGGGCAAGTCAGGACATTGGTATTAAACTTACATTGGCTTCAGCAGGAAC 180
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Qy   181 GATGGAAACTATTAAACGCCTGATCTACGGCCACATCCAGTTGGTTCTGGTGTCCCCAAA 240
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Qy   421 TCCAGTAAGCTTGGG 435
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Db   421 TCCAGTAAGCTTGGG 435
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RESULT 2
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ID AAV83772 standard; cDNA; 435 BP.
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AC AAV83772;
XX
DT 16-MAR-1999 (first entry)
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DE Antibody 11D10 light chain variable region coding sequence.
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KW Murine; mouse; antibody; light chain; variable region; anti-idiotype; ss;
KW human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
XX
OS Mus sp.

Key   Location/Qualifiers
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                 /product= "antibody 11D10 light chain variable region"
                 /transl_except= (pos:163..165, aa:Thr)

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FT mat_peptide   61..435
FT   /*tag= c
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PN WO9856419-A1.
XX
PD 17-DEC-1998.
XX
PF 12-JUN-1998; 98WO-US012250.
XX
PR 13-JUN-1997; 97US-0049540P.
PR 11-JUN-1998; 98US-00096244.
XX
PA (KENT) UNIV KENTUCKY RES FOUND.
XX
PI Chatterjee M, Foon KA;
XX
DR WPI; 1999-060029/05.
DR P-PSDB; AAW87593.
XX
PT Delaying development of, or treating, HMFG-associated tumours - using
PT anti-idiotype antibody 11D10 raised against antibodies to human milk fat
PT globule protein.
XX
PS Disclosure; Fig 1; 54pp; English.
XX
CC This sequence represents the coding sequence for the murine antibody
CC 11D10 light chain variable region. This anti-idiotype antibody is used to
CC delay the development of, or treat, a human milk fat globule (HMFG)
CC associated tumour in an individual having low tumour burden. The antibody
CC 11D10 is used to prevent the recurrence of HMFG-associated tumours e.g.
CC ovarian, non-small cell lung and pancreatic carcinoma, especially for
CC treating breast tumours
XX
SQ Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 U; 0 Other;

Query Match   100.0%; Score 435; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 5.6e-127;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    61 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGACAGAGTCAGT 120
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Db    61 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGACAGAGTCAGT 120

Qy   121 CTCACTTGTCGGGGCAAGTCAGGACATTGGTATTAAACTTACATTGGCTTCAGCAGGAAC 180
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Qy   181 GATGGAAACTATTAAACGCCTGATCTACGGCCACATCCAGTTGGTTCTGGTGTCCCCAAA 240
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Qy   361 GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCA 420
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Qy   421 TCCAGTAAGCTTGGG 435
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

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Searched: 4526729 seqs, 2364849745 residues
Total number of hits satisfying chosen parameters: 9053458
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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
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                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	361.6	83.1	384	10	AB017434	AB017434 Mus muscu
6	361.6	83.1	390	10	MUSIKCC	L41880 Mus musculu
7	352.2	81.0	381	10	AF045508	AF045508 Mus muscu
8	349	80.2	381	10	AF045495	AF045495 Mus muscu
9	345.8	79.5	381	10	AF045510	AF045510 Mus muscu
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11	327.2	75.2	381	10	MMIGGVJ1	X02178 M.musculus
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17	316	72.6	684	10	AB089681	MUSIGKAC1
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23	309.4	71.1	739	6	AR007981	AR007981 Sequence
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25	309.4	71.1	739	6	I23446	I23446 Sequence 5
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28	307.8	70.8	359	10	AY605275	AY605275 Mus muscu
29	307.6	70.7	324	10	MUSX	L48667 Mus musculu
30	307.4	70.7	711	6	E54975	E54975 Peptide. 1/
31	306.4	70.4	324	6	E54967	E54967 Peptide. 1/
32	305.4	70.2	328	10	MMU55591	U55591 Mus musculu
33	305.4	70.2	756	6	AX256284	AX256284 Sequence
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40	298.6	68.6	321	6	MUSIGKAA3	MUSIGKAA3 Mus muscu
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43	296.2	68.1	413	10	MUSIGKCLN	M20832 Mouse IgMk
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ALIGNMENTS

RESULT 1
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LOCUS   AR164505   435 bp   DNA   linear   PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6274143.
ACCESSION   AR164505
VERSION   AR164505.1   GI:16237555
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 435)
  AUTHORS   Chatterjee,M. and Foon,K.A.
  TITLE   Methods of delaying development of HMFG-associated tumors using
            anti-idiotype antibody 11D10
  JOURNAL   Patent: US 6274143-A 1 14-AUG-2001;
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Best Local Similarity   100.0%; Pred. No. 1.9e-120;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION  Methods of delaying development of HMFG-associated tumors using
            anti-idiotype antibody 11D10.
ACCESSION   BD085737
VERSION     BD085737.1  GI:22631347
KEYWORDS    JP 2001523269-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 435)
  AUTHORS   Chatterjee,M. and Foon,K.A.
  TITLE     Methods of delaying development of HMFG-associated tumors using
            anti-idiotype antibody 11D10
  JOURNAL   Patent: JP 2001523269-A 1 20-NOV-2001;
            THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
COMMENT     OS   Unidentified
            PN   JP 2001523269-A/1
            PD   20-NOV-2001
            PF   12-JUN-1998 JP 199903252
            PR   13-JUN-1997 US  60/049540,11-JUN-1998 US   09/096244 PI
            PC   A61K39/395,A61K39/39//C07K16/42
            PA   MALAYA CHATTERJEE,KENNETH A FOON
            PI   Strandedness: Single;
            OS   Topology: Linear;
            CC   Methods of delaying development of HMFG-associated tumors CC
                 using
            CC   anti-idiotype antibody 11D10

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Qy         61 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTGGGACAAAAGAGTCAGT    120
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Db        121 CTCACTTGTCGGGCAAGTCAGGACATTGGTTATTAACTTACATTGGCTTCAGCAGGAACCA    180

Qy        181 GATGGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA    240
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Db        301 GAAGATTTTGTAGCCTATTACTGTCTACAAATATGCTAGTTCTCTCCGTACACGTTCGGAGGG    360

Qy        361 GGGACCAAGCTGGAAATAAAACGGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCA    420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        421 TCCAGTAAGCTTGGG    435
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Db        421 TCCAGTAAGCTTGGG    435
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RESULT 3
LOCUS       E54981                  407 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Peptide.
ACCESSION   E54981
VERSION     E54981.1  GI:18629719
KEYWORDS    JP 2000236884-A/15.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 407)
  AUTHORS   Nishida,T., Okura,T., Tanimoto,T. and Kurimoto,M.
  TITLE     Peptide
  JOURNAL   Patent: JP 2000236884-A 15 05-SEP-2000;
            HAYASHIBARA BIOCHEM LAB INC
COMMENT     OS   Mus musculus (mouse)
            PN   JP 2000236884-A/15
            PD   05-SEP-2000
            PF   24-JUN-1999 JP 199177846
            PR
            PI   TAKEHIRO NISHIDA, TAKANORI OKURA,TADAO TANIMOTO, PI   MASASHI
            KURIMOTO
            PC   C12N15/09,A61K31/00,A61K39/395,A61K48/00,C07K16/24,C12P21/08,
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Matches  393;  Conservative   0;  Mismatches   14;  Indels   0;  Gaps   0;

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Db          1 ATGAGGGGCGCCCCTGCTCAGATTTTTTGGCTTCTTGTTGCTCTGTTGTTCCAGGTACCAGATGT     60

Qy         61 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTGGGACAAAAGAGTCAGT    120
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Qy        121 CTCACTTGTCGGGCAAGTCAGGACATTGGTTATTAACTTACATTGGCTTCAGCAGGAACCA    180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCACTTGTCGGGCAAGTCAGGACATTGGTAGTAAATTATACTGGCTTCAACAGGAACCA    180

Qy        181 GATGGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA    240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA    240
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